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127 RYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSWTGAALS 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 SQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVISIS 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 RDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRG 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  420 LTLSPSQSSNLGVIELPRVHVKDEGEFTCRAQNPLGSQHISLSLSLQNEYIGKMRPISGV 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 LSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWFXAVTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 TIKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYV
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                                                                                                                                                                                                                                                                                                                                               Ig-like lectin-like
HSSP, Q9Y286; 1075.
InterPro; IPR007110; Ig-like.
InterPro; IPR003110; Ig-22.
Pfam; PF00047; ig; 4.
SMART; W000408; igc2; 1.
SMART; W000408; igc2; 1.
SMOST; PS50835; IG LIKE; 3.
Cell adhesion; Glycoprotein; Immunoglobulin domain; Lectin; Repeat; S1gnal; Transmembrane.
SIGNAL
21 597 Sialic acid binding Ig-like lectin-like.
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.larity 41.4%; Pred. No. 1.4e-53;
Conservative 70; Mismatches 164; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Potential.
Cytoplasmic (Potential).
Gytoplasmic (Potential).
Ig-like V-type 1.
Ig-like C2-type 1.
Ig-like C2-type 2.
ITIM motif.
Ig-like C2-type 2.
ITIM motif.
By similarity.
By similari
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SEQUENCE
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STRAIN=CZECH IN.

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C STRAIN=CZECH IN.

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C EXPression driven metastatized to lung. MMTV-LTR/Wnt1 model.

EXPRESSION driven by an MMTV-LTR enhancer.

C EXPRESSION driven by an MMTV-LTR enhancer.

C EXPRESSION driven by an MMTV-LTR enhancer.

C STRAIN=CZECH IN.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MILDFLLSSLIGGSQAMDGR----FWIRVQESVMVPEGLCISVPCSFSYPRO---DWTG
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39.0%; Pred. No. 1.4e-51;
ive 75; Mismatches 170; Indels 74; Gaps
                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Makaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCB_TaxID=10090;
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TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
Expression driven by an MMTV-LTR enhancer.;
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EMBL, BC023280; AAH3280.1; -.
GO, GO:0004872; F:receptor activity; IDA.
GO:0005057; F:receptor signaling protein activity; IPI.
GO; GO:0007155; F:receptor signaling
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InterPro; IPR00710; Ig-11ke.
InterPro; IPR00710; Ig-11ke.
InterPro; IPR003598; Ig_C2.
InterPro; IPR0040; Ig_MHC.
SWART; SW00409; IG-2; I.
PR0571F; PS00409; IG-2; I.
PR0571F; PS00989; IG-2; I.
PR0571F; PS00989; IG-MHC; UNKNOWN I.
SEQUENCE 468 AA; 51987 MW; 26A0FF74D3CA4ACF CRC64;
                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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                                                                                                                                                                 Created)
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                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                               Name=Siglecl1;
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05-JUL-2004
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Q6PJ50;
RESULT 12
Q6PJ50
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39.0%; Pred. No. 1.4e-51;
tive 75; Mismatches 170; Indels
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                                                                                                                                                                                                                                                                                                                                                                   AAQ72479;
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Sialic acid binding 19-like lectin E.
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                                            238 NVSYAPK----
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SEQUENCE FROM N.A.
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SEQUENCE
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                                            113 ESQYFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEE 172
                                                                                                                                                                                                                                                                                281
                                                                                                                                                                                                                                                                                                                            293 HSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSV 352
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                                                                         238 NVSYAPK-------NLTVTIYQGADSVSTILKNGSSLPISEGQSLRLICST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  342 QSSATL--SEMMGTFVGSGVTALLFLSVCILLLAVRSYRRPARPAVVAPHP-----
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                                                                                                                                                                                   180 TAPPIFSWIGTSVSFLSTNTIGS -- SVLTITPQPQDHGTNLTCQVTLPGTDVSTRMTIRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSST
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                                                                                                                                                                                                                               RVAYAPRDLVISISRDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGOSLCLVCVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Sialic acid binding immunoglobulin-like lectin-E.
Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 32.4%; Score 878; DB 2; Length 46
Best Local Similarity 39.0%; Pred. No. 1.4e-51;
Matches 204; Conservative 75; Mismatches 170; Indels
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STRAIN=C5/BL/6;
Zhang J.Q., Crocker P.R.;
"Characterization of mSiglecs-E and -F.";
Submitted (UUL-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                                  282 DSYPPANLSWSWDNLTLCPSKLSKPGLLELFPVHLKHGGGVYTCQAQHALGSQHISLSLSP
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   -----NLTVTIYQGADSVSTILKNGSSLPISEGQSLRLICST
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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TISSUB-Mammary tumor metastatized to lung. MMTV-LTR/Wntl model.

Expression driven by an MMTV-LTR enhancer;

MEDINE-22388257; PubMed-1247932;

Attausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Attausherg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J. Usdin T.B., Tonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Morley K.C., Hale S., Garcinci P., Prange C.,

Richards S., Worley K.C., Hale S., Garcinci P., Prange C.,

Whilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glibbs R.A.,

Fahey J., Helton B., Ketteman M., Madan A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevorchenko Y., Bouffard G.G.,

Makesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Sochein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                          409 ILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSST 468
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342 QSSATL--SEMWAGTFVGSGVTALLFLSVCILLLAVRSYRKPARPAVVAPHP-----
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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TIESUE=Mammary tumor metastatized to lung. MMTV-LTR/Wntl model.
Expression driven by an MMTV-LTR enhancer;
Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC023280, AA123280.1;
SEQUENCE 468 AA; 51987 MW; 26AOFF74D3CA4ACF CRC64;
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Last annotation update)
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Search completed: November 5, 2004, 13:57:39 Job time : 116.542 secs

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121 AGLYFFRLERGK-TKYNYMMDKMTLVVTALTNTPQIILPETLEAGHPSNLTCSVPWDCGW 179
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32.8%; Score 888; DB 3; Length 43:
Best Local Similarity 47.8%; Pred. No. 1.5e-69;
Matches 195; Conservative 52; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-038-832-2

Sequence 2, Application US/09038832

Sequence 2, Application US/09038832

Sequence 2, Application US/09038832

Sequence 2, Application US/09038832

PAPLICANT: EXISTINE

APPLICANT: EXISTINE

TITLE OF INVENTION: (SAF-2)

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSE: RATHRER & PRESTIA

STREET: P.O. BOX 980

CITY: VALLEY PORGE

STATE: PA

COUNTRY: USA

ZIP: 19482
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,832
FILING DATE: 11-MAR-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/041,886
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESENCE/DOCKET NUMBER: 23,031
REFERENCE/DOCKET NUMBER: 23,031
REFERENCE/DOCKET NUMBER: 23,031
TELECOMMUNICATION INFORMATION:
             US-09-778-510-2
US-08-78-510-2
US-08-778-510-14
US-09-778-510-6
US-09-90-778-510-6
US-09-90-778-84-84
US-09-90-778-84-84
US-09-906-705-84
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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amino acid
TOPOLOGY: linear; MOLECULE TYPE: protein US-09-038-832-2
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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- 2004 Compugen Ltd.
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Result No.

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REGISTRATION NUMBER: 23,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        610-407-070
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: P.O.
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                                                           Similarity
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TELEX:
US-09-038-832-4
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                                        Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                 239 VRLDVSY-----PPWNLTMTVFQGDATASTALGNGSSLSVLEGQSLRLV 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                283 CAVNSNPPARLSWIRGSLILCPSRSSNPGLLELPRVHVRDEGEFICRAQNAQGSQHISLS 342
                                                                                 55 PAYGYWFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDES 114
                                                                                                                   61 PVHGYWFRAGDRPYQDAPVATNNPDREVQAETQGRFQLLGDIWSNDCSLSIRDARKRDKG 120
                           1 MLILILILIPLINGTKGMEGDRQYGDGYLLQVQELVTVQEGLCVHVPCSFSYPQDGWTDSD 60
  MLLPLLLSSLLGGSQAMDG-----RFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGST 54
                                                                                                                                                                                                                                           170 FEECPPSFSWIGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRT
                                                                                                                                                                                                                                                                                                                          230 VRLRVAYAPRDLVISISRDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KIKLY, KRISTINE
APPLICANT: BRICKSON-MILLER, CONNIE
TITLE OF INVENTION: Sialoadhesin Family Member-2
TITLE OF INVENTION: (SAF-2)
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAINER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastGED for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JNBER: US/09/038,832
11-MAR-1998
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APPLICATION NUMBER: 60/041,886
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Requence 4, Application US/09038832
Ratent No. 6146845
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IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       431 amino acids
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REGISTRATION NUMBER:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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STRANDEDNESS: single
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COMPUTER READABLE FORM:
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170 FEBCPPPSFSWTGAALSSQGTKPTTSHPSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRT 229
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                                                                                                                           1 MILPILLSSILGGSQAMDG-----RFWIRVQESVMVPEGLCISVPCSFSYPRQDWIGST
                                                                                                                                                                                       1 MILILILILILIPLIMGTKGMEGDRQYGDGYLLQVQELVTVQEGLCVHVPCSFSYPQDGWTDSD
                                                                  34; Gaps
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      Length 431;
32.8%; Score 888; DB 3; Length 43:
llarity 47.8%; Pred. No. 1.5e-69;
Conservative 52; Mismatches 127; Indels
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Patent No. 6090582
GENERAL INFORMATION:
APPLICANT: KIKLY, KRISTINE
APPLICANT: KIKLY, KRISTINE
TITLE OF INVENTION: SIAloadhesin Family Member-3
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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SOFTWARE: FastSEQ for Windows Version 2.0
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APPLICATION NUMBER: US/09/046,736
FILING DATE: 24-MAR-1998
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/041,885
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
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121 ERGRDVKYSYQQNKLNLEVTALIEKPDIHFLEPLESGRPTRLSCSLPGSCEAGPPLTFSW 180
                                                                                                                                                                                                                                                                                                                                                        --GIGITALLFLCLALIIM 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             387 KILPKRRTQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPL-PPGAPS 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                460 LIVKARRKĢA-AGRPEKMDDED------PIMGTITSGSRKKPWPDSPGDQASPPGDAP 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 LVISISRDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGOSLCLVCVTHSSPPARL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          340 PSCSWEAEGLHCRCSFRAWPAPSLCWRLEEKPLEGNSSOGSFKVNSSSPGPWANSSLILH 399
                                                                                                                                                                                                                                                                       301 SWIORGOVLSPSOPSDPGVLELPRVOVEHEGEFICHARHPLGSOHVSLSLSVHYKKGLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          446 PESKKNQKKQYQLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQA-
                                                                                         61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
                                                                                                                                                                    ERGSYVRYNFWNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW
                                                                                                                                                                                                                                                 TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
              LIPLILSSIL-GGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
                                                 1 MIPLILLPLIMGGSLQEXPVYBLQVQKSVTVQEGLCVLVPCSFSYPWRSWYSSPPLYVYW
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Patent No. 6225446
GENERAL INFORMATION:
APPLICANT: Altmann, Scott W.
APPLICANT: Rack, Fernando L.
APPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMMLIAN PROTEINS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release L1
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CLASSIFICATION: 435
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STATE: California
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US-08-759-628-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YAPRDLVISISRDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSS 295
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                                                                                                                                                                                                                                                                                            56 AYGYWFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQ 115
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                                                                                                                                                                                                               2 LIPILLISSILGGSQAMDGR----FWIRVQESVMVPEGLCISVPCSFSYPRODWTGSTP
                                                                                                                                                                                                                                                                                                                                                                       116 YFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              341 YTGKMRPVSGVLL----GAVGGAGATALVFLSFCVİFIVV---RSCRKKSARP----
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                                                                                                                                    Length 467;
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                                                                                                                                  Score 831.5; DB 3; Length
Pred. No. 1.5e-64;
3; Mismatches 174; Indels
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29.6%; Score 800.5; DB 4;
Best Local Similarity 33.7%; Pred. No. 1e-61;
Matches 205; Conservative 71; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08896537A
Patent No. 659008B
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Gentz, Reiner L.
APPLICANT: Gentz, Reiner L.
TITLE OF INVENTION: CD33-Like Protein
FILE REFRENCE: 1488 048001
CURRENT APPLICATION NUMBER: US/08/896,537A
CURRENT FILING DATE: 1997-07-18
FRIOR APPLICATION NUMBER: 60/022,481
FRIOR APPLICATION NUMBER: 60/022,481
FRIOR APPLICATION NUMBER: 60/022,481
FRIOR APPLICATION NUMBER: 0507-07-18
FRIOR APPLICATION NUMBER: 07-07-18
FRIOR FILING DATE: 1996-07-19
NUMBER OF SEQ ID NOS: 12
                                                                                                                                  Query Match
Best Local Similarity 37.9%; Pr
Matches 198; Conservative 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               387 ----AADVGDVGMK---
467 amino acids
                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                        , MOLECULE TYPE: protein US-09-046-736-2
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ORGANISM: Homo sapiens
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US-08-896-537A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 YAPRDLVISISRDNTFDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSS 295
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APPLICANT: Rock, Fernando L.
APPLICANT: Rock, Fernando L.
APPLICANT: Razan, J. Fernando
APPLICANT: Kastejein, Robert A.
TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMMLIAN PROTEINS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 28.4%; Score 769; DB 3; Length 440; SBest Local Similarity 36.5%; Pred. No. 4.3e-59; Matches 190; Conservative 73; Mismatches 163; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      471 PESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK 510
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                                                                                                 NAME: Ching, Edwin P.
REGIGTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0552Q
TELECOMMUNICATION INFORMATION:
TELERENONE: 415-852-9196
TELERENONE: 415-496-1200
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Patent No. 6225446
GENERAL INFORMATION:
                                           FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                            440 amino acids
                                                                                                                                                                                                                             TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein US-08-759-628-4
PRIOR APPLICATION DATA: APPLICATION NUMBER:
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MS-08-759-628-5
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RGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPG--QPVTVICVFNWAFEECPPPSFS 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RDGEIPYYAEVVATNNPDRRVKPETOGRFRLLGDVOKKNCSLSIGDARMEDTGSYFFRVE 120
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                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.6%; Score 693.5; DB 3
43.0%; Pred. No. 1.7e-52;
                                                                                                                                                                                                                                                                                             CLASSIPACATION DATA:
APPLICATION NUMBER: US 60/008,574
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTATION NUMBER: 34,090
REFERRUCE/DOCKET NUMBER: DX05520
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                       UMBER: US/08/759,628
05-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 421 amino acids
amino acid
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APPLICANT: Gentz, Reiner L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO:
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MOLECULE TYPE: protein
                                                                ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                        California
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Best Local Similarity
Palo Alto
                                                                                                                                                                                                                                                        FILING DATE: 05
CLASSIFICATION:
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                                               USA
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                                            COUNTRY:
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Diskette

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MEDIUM TYPE:
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                                                                                                                                                                                                                                                           Query Match 25.6%; Score 693; DB 4; Length 364; Best Local Similarity 33.2%; Pred. No. 1.5e-52; Matches 170; Conservative 59; Mismatches 135; Indels 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09046736
Patent No. 6090582
GENERAL INFORMATION:
APPLICANT: KIKLY, KRISTINE
FILICANT: ERICKSON MILLER, CONNIE
TITLE OF INVENTION: Sialoadhesin Family Member-3
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rather & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481 HYATLNFPGVRPRPEARMPKGTQADYAEVKFQ 512
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APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: CD31-Like Protein
FILE REFERENCE: 1488 0480001
CURRENT APPLICATION NUMBER: US/08/896,537A
CURRENT FILING DATE: 1997-07-18
FRIOR APPLICATION NUMBER: 60/022,481
PRIOR FILING DATE: 1996-07-19
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                             364
                                                                                                                                                                                                                              US-08-896-537A-3
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US-09-046-736-4
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296 PPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYK 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 YAPRDLVISISRDNTFDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSS 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSS 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294 -----AADVGDIGMK-------DANTIRGSASQGNLTESWADDNPRHH 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 YIGKWRPVSGVLL----GAVGGAGATALVFLSFCVIFIVV---RSCRKKSARP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 AYGYWFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 PPARLSWTWRSLTLYPSQPSNPLVLEL-QVHLGDEGEFTCRAQNSLGSQHVSLNLSLQQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 LLPLLLSSLLGGSQAMDGR-----FWIRVQESVMVPEGLCISVPCSFSYPRODWTGSTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 YFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVXIPETLEPGQPVTVICVFNWAFEECPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 21.2%; Score 573; DB 3; Length 374;
Best Local Similarity 29.8%; Pred. No. 5.4e-42;
Matches 156; Conservative 63; Mismatches 138; Indels 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      468 TQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK 510
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COMPUTER: IBM Compatible
COREATING SYSTEM: DOS
SOFTWARE: FASESEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,736
FILING DATE: 24 WAR-1998
CLASSIFICATION: 214
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/041,885
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/POCKET NUMBER: 33,031
REFERENCE/POCKET NUMBER: GH-50019
TELECONMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7159, Application US/09513999C Patent No. 6783961
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
TYPE: amino acid
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80 IQNPMPIREGDTVTLSCNYNSSNPSVTRYEW----KPHGAWEEPSLGVLKIQNVGWDNTT 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 REVEMSTRGREGLTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYVRYNFMNDGFFLKV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 TALTOKEDVYIPETLEPGOPVTVICVENWAFEECPPPSFSW--TGAALSSOGTKPTTSHF 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              292 PHHSQKLRLEPVKVQHSGAYWCQGTNSVGKGRSPLSTLTVYYSPETI-----GRRVAVG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         346 LGS----CLAILILLAICGLKLQRRWKRTQSQQGLQENSSGQSFFVRNKKVRRAPLSEGPH 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 SVLSFIPRPODHDIDLICHVDFSRKGVSAQRIVRLRVAYAPRDLVISISRDNIPDPPENL 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258 RVMVSQANRTVLENLGNGTSLPVLEGOSLCLVCVTHSSPPAR----LSWTQRGQVLSPSQ 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259 -----SL 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            373 ITALLFLCLALLIMKI----LPKR--RTQTET-------PRPRFSRHSTILDYIN 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 VQESVMVPEGLCISVPCSF----SYPRQDWTGSTPAYGYWFKAVTBTTKGAPVATNHQS 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 KPLSE-----IHSGNSVSLQCDFSSSHPK--EVQFFWEXNGRLLG----KESQLNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 501;
1 MILPELLESSILGGSQAMDGRFWIRVQESVWVPEGLCISVXLLPLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NOTA:
APPLICATION NOTA:
APPLICATION NOTA:
APPLICATION NOTA:
APPLICATION NOTA:
APPLICATION NOTA:
ALASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MACK, Susan J.
RECISTRATION NOTABER: 30,951
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                  APPLICANT: Chinnadurai, Govindaswamy
TITLE OF INVENTION: APOPTOPSIS-REGULATING PROTEINS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS STREET: 2100 Pennsylvania Avenue, N.W. CITY: Washington STATE: D.C. COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guery Match 6.6%; Score 177.5; DB ; Best Local Similarity 20.0%; Pred. No. 4.3e-07, Matches 107; Conservative 82; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                       Sequence 31, Application US/08408095
Patent No. 5858678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 501 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                       -08-408-095-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                         APPLICANT: Duciert, A.
APPLICANT: Glordano, J.Y.
ATTLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
ETLE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
AUMBER OF SEQ ID NOS: 36681
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APPLICANT: Dunas Milne Edwards, J.B.

APPLICANT: Duclert, A.

APPLICANT: Duclert, A.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

PACHEL NO. 6783561

PALER REFERENCE: 59.US2.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 2000-02-24

PRIOR PILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYP 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION: seq PLLLSSLLGGSQA/MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . Sequence 4599, Application US/09513999C . Patent No. 6783961
                            : Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Xaa=His or Gln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Xaa=Ala or Ser
US-09-513-999C-4599
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                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patent.pm
SEQ ID NO 4599
LENGTH: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: -16..-1
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: UNSURE
LOCATION: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: SIGNAL
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NAME/KEY: UNSURE
LOCATION: 24
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-09-513-999C-4599

TYPE: PRI

OTHER

08-09-513-999C-7159

SEQ ID NO 7159

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GENERAL INFORMATION
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APPLICANT: Stern, David M.
APPLICANT: Stern, David M.
APPLICANT: Schmidt, Ann Marie
APPLICANT: Schmidt, Ann Marie
APPLICANT: Schmidt, Ann Marie
TITLE OF INVENTION: TRANSCENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
TITLE OF INVENTION: 0555/6215
CURRENT APPLICATION NUMBER: US/09/638,649
CURRENT FILING DATE: 2000-08-14
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                                                       461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 GOPVTV-ICVFNWAFEECPPPSFSW--TGAALSSQGTK------PTTSHFSVLS-F 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 EPEGGI-------VAPGGTVTLTCAISAQPPPQVHWIKDGAPL-PLAPSP--VLL 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         322 LPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHY-------KKGLISTAFSNGA 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  368 FLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINVVPTAGPLAQKRN 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----VGAILWRKR 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            428 QKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPESQESQEELHYATLNF 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----APESQEDEEE--RAELN- 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 SVPNKVGTCVSEGSY---PAGTLSWHLDGKLLIPDGKETLVKEETRRHPETGLFTLRSEL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 TVIPTOGGTTHPTFSCSFS-LGLPRRRPLNT----APIQL-----RVREPGPPEGIQLLV 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQANRIVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLE 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 NCSLVIRDAQMQDESQYFFRV--ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPET-LEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPRP-QDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVISISRDNTPDPPENLRVMV
                                                     102 SLGCYNPMMEDGISYTTLRFPEMNIPRTGDAESSEMQRPPRTCDDTVTYSALHKRQVGDY
                                                                                        Q--LPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPRPRARMPKGTQADYAEVK 510
                                                                                                                    46; Mismatches 139; Indels 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.4%; Score 172.5; DB 4; Length 403; 23.3%; Pred. No. 8.7e-07;
                 415 VVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESK-
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                                                                                                                                                                                                                     Sequence 5, Application US/09638649
Patent No. 6563015
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                                                                                                                          462 ENVIPOFPE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 101; Conserv
                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Stern,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 5
LENGTH: 403
                                                                                                                                                                                 RESULT 12
US-09-638-649-5
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                                                                                        457
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RESULT 13 US-08-602-725-32 'Sequence 32, Application US/08602725 'Patent No. 5965/10

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110 MQDESQYFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 GY-WFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKG-----NCSLVIRDAQ 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 -RLOLSNGRITLILLSVTRNDTGPYECEIQNPVS-ANRSDPVTLNVTYGPDTPIISPSDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 LLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVP-----CSFSYPRQDWTGSTPAY
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                                                                                                                                                        TITLE OF INVENTION: MONOCLONAL ANTIBODIES FOR USE IN
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
TUTLE OF INVENTION: DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.2%; Score 167; DB 2; Length 464; Best Local Similarity 23.5%; Pred. No. 3.2e-06; Matches 85; Conservative 52; Mismatches 122; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 QNDTGFYTLQV----IKSDLVNE-----EATGQFHVY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin 1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,725
FILING DATE: 02-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB94/01816
FILING DATE: 19-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9317423
FILING DATE: 21-AUG-1993
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: SADOFP, B.J.
REGISTRATION NUMBER: 36663
REFERENCE FOCKET NUMBER: 10
TELECOMMINICATION INFORMATION:
TELEPHONE: 703-816-4091
                                                  SNARY, DAVID
STEWART, LORNA MD
YOUNG, SUSAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 32: SEQUENCE CHARACTERISTICS: LENGTH: 464 amino acids
WALTER
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amino acid
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) MOLECULE TYPE: protein
US-08-602-725-32
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MEDIUM TYPE: Floppy
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                                                  APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Stern, David M.
APPLICANT: Stern, David M.
APPLICANT: Stern, Ann Marie
APPLICANT: Yan, Shi Du
TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
FILLE REFERENCE: 05/5/62175
FULB REFERENCE: 05/5/62175
CURRENT APPLICANTION NUMBER: US/09/638,649
CURRENT FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 -PELPKPS-----ISSNNSNPVEDKDAV-AFTCEPETODTTYLWWINNQSLPVSP--- 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       283 ----GOSICIVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHAR 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 YYRPGANLSLSCYAASNPPAQYSWLINGTFQQSTQE-----LFIPNITVNNSGSYTCHAN 302
 248 YYRPGANLSLSCYAASNPPAQYSWLINGTFQOSTQE-----LFIPNITVNNSGSYTCHAN 302
                                                                                                                                                                                                                                                                                                                                                                                                                                         58 GY-WEKAVIETIKGAPVATNHOSREVEMSTRGRFQLTGDPAKG-----NCSLVIRDAQ
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                                                                                                                                                                             APPLICANT: WAI-YEE, CHAN
TITLE OF INVENTION: PREGNANCY SPECIFIC PROTEINS APPLICATIONS
NUMBER OF SEQUENCES: SEQUENCES: CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/390,409
FILING DATE: 07-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                     Length 321;
                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.7%; Score 155; DB 6; Length 321 gest Local Similarity 24.3%; Pred. No. 2.2e-05; Matches 73; Conservative 43; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 ONDIGEYTLOV----IKSDLVNE-----EATGOFHVY---
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Patent No. 6563015
GENERAL INFORMATION:
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, ORGANISM: BOS Tauris
US-09-638-649-1
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Best Local Similarity
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US-09-638-649-1
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SEQ ID NO 1
LENGTH: 416
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169835-17
Patent No.
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                                                                                                                                                                                                                                      166 FNWAFEECPPPSFSW--TGAALSSQG-----TK--PITSHF---SVLSFTPRPQDHD 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303 PEDQGTYSCVATHPSHGPQESRAVSVTIIETGEBGTTAGSVBGPGLETLALTLGILGGLG 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   373 ITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKATP 432
                                                                                                                                                                                                                                                                                                                                                                                       145 SEGGY---PAGTLNWLLDGKTLIPDGKGVSVKEETKRHPKTGLFTLHSELMVTPARGG-- 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                     211 TDLTCHVDFS---RKGVSAQRTVRLRVAYAPRDLVISISRDNTPDPPENLRVMVSQANRT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---ALHPTFSCSFTPGLPRRRALHT----APIQLRVWSEHRGGEGP--NVDAVPLKEVQL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268 VLENLGNGTSLPVLEGOSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPG-VLELPRVQ 326
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                                                                                                                        32 KPLVLNCKGAP-KKPPQQLEWKLNT-GRTEAWKVLSPQGDPWDSVARVLPNGSLLLPAVG 89
   57; Mismatches 170; Indels 125; Gaps
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                                                                 62 KAVTETTKGAPVATNHQSREVEMSTRGRFQL-----TGDP---
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      108; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: November 5, 2004, 13:50:17; Search time 14.2346 Seconds (without alignments)
3460.797 Million cell updates/sec

Title: US-09-937-636-3
Perfect score: 2706
Sequence: 1 MilplilsSilgGSQAMDGR......RPEARMPKGTQADYAEVKFQ 512

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Total number of hits satisfying chosen parameters: 283416

283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	myeloid cell surfa	soform	ģ	cell	in-associ	myelin-associated	in-associ	sialoadhesin - mou	differentiation an	CD22 homolog/B lym	B-cell adhesion pr	11 adhesion	റ	able	perlecan precursor	biliary glycoprote	biliary glycoprote	biliary glycoprote	transmembrane carc	pregnancy-specific	heparan sulfate pr	advanced glycosyla	nephrin - human	>		hypothetical prote		myosin-light-chain	pecif
SUMMARIES	Ω	1 2	152590	90	•	BNRT3	m	B33785	10	m	_	•	\sim	A32164	10	$\boldsymbol{\sigma}$	φ	9	3,9	12	C27658	S	87	9	112	245	δ	329	823	900
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d	Query Match	. 5	19.5	ä	ä	ö	ö	٥.			•	•			•			•		•							S.			
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titin, cardiac mus	carcinoembryonic a	neural cell adhesi	vascular cell adhe	pregnancy-specific	poliovirus recepto	poliovirus recepto	pregnancy-specific	pregnancy-specific	biliary glycoprote	Lutheran blood gro	pregnancy-specific	advanced glycosyla	carcinoembryonic a	pregnancy-specific	Cificana - Vonennard
I38344	A36319	T43027	JN0581	A54312	RWHUPD	RWHUPA	I57486	JS0032	834338	I38000	JC4123	I61596	A34815	A55181	74774
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144.5 5.3 26926 1	5.3		5.2		5.2	5.2		5.2	5.2		5.2		5.1		r L

ALIGNMENTS

RESULT 1 A30521	
myeloid c C;Species C;Date: 0 C;Accessi	myveloid ceil surface antigen CD33 precursor - human G;Species: Homo sapiens (man) C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004 C;Accession: A30521
R; Simmons J. Immuno A; Title: A; Referen	Risimmons, D.; Seed, B. J. Immunol. 141, 2797-2800, 1988 A;Title: Isolation of a CDNA encoding CD33, a differentiation antigen of myeloid progenit A;Reference number: A30521; MID:89009814; PMID:3139766
 A; Accessi A; Molecul A; Residue	A;Accession: A30521 A;Molecule type: mRNA A;Residues: 1.364 <sim></sim>
 C;Genetics: A;Gene: GDB:CD33 A;Cross-referenc	s: DB:CD33 eferences: GDB:119762; OMIM:159590
 A; Map pos C; Keyword F:1-17/Do	ition: 19q13.3-19q13.4 s glycoptothin surface antigen; transmembrane protein main: signal semiance #status pradicted 2873.
F; 18-259/ F; 260-282 F; 283-364	=
Filovilis, too Query Match Best Local Matches 16	100,113,150,209,230/Dimining site: carbonyquate (ABM) (COVAIEM) #Status predicted Query Match 25.6%; Score 694; DB 2; Length 364; Best Local Similarity 32.8%; Pred. No. 1e-39; Matches 168; Conservative 59; Mismatches 137; Indels 148; Gaps 8;
à t	MILPLILSSLIGGSOAMDGREWIRVOBSVAVPBGLCISVPCSFSYPRODWTGSTF
8 8	
Db	61 FREGALISGOSPVATNKLDGEVQEETQGRFRLLGDPSRNNCSLSIVDARRRDNGSYFFRM 120
ठे द	121 ERGSYVRYNEMNDGFELKVTALTOKPDVYIPETLEBGOPVTVICVFNWAFBECPPESFSW 180 121 BGC - TRYGYGVK CDGI, SI, MIT
ì à	TGAALSŞQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
 Ωp	180 LSAAPTSLGPRTTHSSVLITTPRPQDHGTNLTCQVKFAGAGVTTERTIQLNVTYVPQN 237
 à	241 LVISISRDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARL 300
 Db	238 PTTGIFP 247
 ò	301 SWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYKKGLIS 360
 Db	248SGKQETRAGVV 258

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human myelin-associated glycoprote
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F;18-120/Region: cell attachment (R-G-D) motif F;18-130/Region: cell attachment (R-G-D) motif F;14-536/Domain: transmembrane #status predicted <TWM>
F;194-536/Domain: transmembrane #status predicted <TWM>
F;195-323,246,315,406,450,454/Rinding site: carbohydrate (Asn) (covalent) #status predicted respectively first site: carbohydrate (Asn) (covalent) #status predicted F;343,807/Binding site: phosphate (Ann) (covalent) #status predicted F;313/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Residues: 84-98, xx, 100-110,210-222, xx, 224,245, xx, 247-253,309-318, xxxx, 396-405, xxx
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 KGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYVRY 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 VIVEMNSSVEAIEGSHVSLLCGADSNPPPLLTWMRDGTVLREAVAESLLLELEEVTPAED 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----SQANRIV-----LENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSW 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYKKGLI--- 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             420 HCAAARDTVQCLCVVKSNPEPSVAFELPSRNVTVNESEREFVYSERSGLVLTSILTL--- 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FWIRVO-------BSVMVPEGLCISVPCSFSYPRODWTGSTPAYGYWFKAVTETT 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---AALSS-QGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----STAF -----SNGAFL ----GIGITALLFLCLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 FWIMISASRGGHWGAWMPSSISAFEGTCVSIPCRPDFP--DELRPAVVHGVWYFNSPYPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 NEWNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPP--PSFSWTG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------PENLRVMV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.3%; Score 304.5; DB 1; Length 626;
21.1%; Pred. No. 4.9e-13;
ive 90; Mismatches 229; Indels 193; Gaps
                                                                                                                                                                                                                                                                                                                A,Cross-references: GB.M29273, NID:g187292; PIDN:AAA59545.1; PID:g307156 R; Burger, D.; Pidoux, L.; Steck, A.J.
Biochem. Biophys. Res. Commun. 197, 457-464, 1993 A; Title: Identification of the glycosylated sequons of human myelin-assoc A; Reference number: PC2011; MUID:94092116; PMID:7505568
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                                                                                                                                                                                                        Reference number: A33263; MUID:89392063; PMID:2476987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: GDB:120702; OMIM:159460
                                                                                                                                                                                                                                                                  Molecule type: mRNA;Residues: 1-613,'T',615-626 <SAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Map position: 19q13.1-19q13.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 21.18
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: GDB:MAG; GMA
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A) Accession: 152590
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"Regidues: 1-626 <SPA>
"Cross-references: UNIPROT:P20916
"Sato, S.; Fujita, N.; Kurihara, T.; Kuwano, R.; Sakimura, K.; Takahashi, Y.; Miyatake,
"Jacchem. Biophys. Res. Commun. 163, 1473-1480, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          myelin-associated glycoprotein precursor - human
C,Species: Homo sapiens (man)
C,Date: 31-Dec-1993 Heguenoc revision 16-Aug-1996 #text_change 09-Jul-2004
C,Accession: A61084, A33263; Pc2011
R,Spagnol, G.; Williams, M.; Srinivasan, J.; Golier, J.; Bauer, D.; Lebo, R.V.; Latov, J. Newsoci. Res. 24, 137-142, 1989
M.; Marcoci. Res. 24, 137-142, 1989
M.; Litle: Molecular cloning of human myelin-associated glycoprotein.
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                                                                                                                                                                                                                                                                                                    304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .21 ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59
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මාමුන්ප: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 TAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINVVPTAG
                                                                                                                                                                                                                                                                                                                                                          421 PLACKRNOKATPNSPRTPLPPGAPSPESKKNOKKOYQLPSFPEPKSSTQAPESQESEL
                                                                                                                                                                                                                                                                                                                                                                                                                 --TETSSCSGAAPTVEMDEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MIMPLPLFLLCAGSLAQDLEFQLVAPESVTVEEGLCVHVPCSVFYPSIKLT-LGPVTGSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: GB:871345; NID:g551352; PIDN:AAB30842.1; PID:g551353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 LVISISRDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLV 289
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42.2%; Pred. No. 2.1e-28;
tive 34; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                    ----HGAIGGAGVTALLALCLCLIFFIVKTHRRKAARTAVGRNDTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .; Beverley, P.C.; Young, B.D.; Watt, S.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Status: preliminary; translated from GB/EMBL/DDBJ
A Molecule type: mRNA
A Residues: 1-403 <RES>
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Matches 122, Conservative
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Refebilian, E.Z.; Beverley
Blood 83, 3188-3198, 1994
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OY 462 PEPKSSTQAPESQESQEBLHYATLNFPGVRPRPEARMPKGTQADYAEVK 510 DD 587RGEPPELDL6YSHSDL-GREPTKSSYTLSEELABYAEIR 624	Qy 407STILDYINVPTAGPLAQKENQKATPNSPRTPLPPGAPSPESKKNQ 452 Db 514 VGPVGAVAFAIVIAVVCXISQSRRKKGAGSPEVTPVQPNAGPGGDPDLDLRPQQVRWLR 573
RESULT 4	453KKQYQLPSFPEPKSSTQAPESQESQESGEEHYATLNFPGVRPRPEARMPKGTQADYAEVK
nge 09-Jul-2004	DD 574 GAMEKWALGVREGSGAFQEVIFISHFFRRFIKGFLEDFFEIABIK 010 RESULT 5 BNRT3
larshak, D.R.; Roder, J.; Le	myelin-associated glycoprotein precursor, long splice form - rat Nighternate names: 18256, brain neuron cytoplasmic protein 3; MAG
in procein, SMF: structural	C.Species: katcus norvegicus (Norway Lat.) C.bate: 19-Feb-1984 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004 C.Accession: A29028, A94175, ĀZ7185, A908564, I52892, A03138, A26362 R:Lat. C.: Brow. M.A.: Nave. K.A.: Noronha. A.B.: Ouarles, R.H.: Bloom. F.E.: Milner, R.L
A;Residues: 1-620 cDUL> A;Residues: 1-620 cDUL> A;Cross-references: UNIPROT:Q92154; GB:S83711; NID:g245729; PIDN:AAB21466.1; PID:g24573d A;Experimental source: spinal cord A;Note: the species of quail is not identified	Ęo
ם בי מיהמילית איר מים מים בי מים מים מים מים מים מים מים מים מים מי	A;Molecule type: mRNA A;Residues: 1-626 <lai> A;Cross-references: UNIPROT:P07722; GB:MI6800; NID:g205269; PIDN:AAA41557.1; PID:g205270 B:arminf M Poder I Chia I S Down I Wilkinson D: Bayley H.: Braun P.: Dur</lai>
n homology	oteir
mental <sch></sch>	A, Accession: A94175 A, Molecule Type: milky A, Donidine Type: milky
lent) #status predicted	A.Cross-references: GB:M14871; NID:g205267; PIDN:AAA41556.1; PID:g205268 R;Salzer, J.L.; Holmes, W.P.; Colman, D.R.
Query Match 11.2%; Score 302.5; DB 2; Length 620; Best Local Similarity 22.4%; Pred. No. 6.6e-13; Matches 148; Conservative 89; Mismatches 224; Indels 199; Gaps 29;	J. Cell Biol. 104, 957-965, 1987 A;Title: The amino acid sequences of the myelin-associated glycoproteins: homology to the A;Reference number: A27185; WUID:87166195; PMID:2435742
LLLSSLLGGSQAMDGRFWIRVQSSVAVPEGLCISVPCSFSYPRQDWTGSTPAYGYWFK 6	
4 LVLTVLLMGTGCISAPWAAMMPPKWAALSGTCVQLPCRFDYPEBLRPASIGGLWY- 58 63 AVMETTKGAPVATWHOSREVEWSTRGFFOLTGDPAKGNCSLVTRDAOMODE- 113	A;Cross_references: GB:X05301; NID:g56611, PIDN:CAA28920.1; PID:g56612 R;Sutcliffe, J.G.; Milner, R.J.; Shinnick, T.M.; Bloom, F.E. Cell 33, 671-682, 1983
FGSPYPKNYPPVVARSRPSSAVHESFAGRASFLGDPTGRDCTLNIARLSEBL 110	A,Title: Identifying the protein products of brain-specific genes with antibodies to chem A,Reference number: A90836; MUID:83259254; PMID:6347394
114 -SQYFERVERGSYVRYNFWNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEE 172	Ajaccession: Ajosjo Ajaccessione: 'KS',311-626 <sut> Ajacserreferences: GR-VOLIA44 GR-JOO756. NID-GE6879. PIDN.CAA24786.1: PID-G818027</sut>
CPPPSFSWTGAALSSQGTKPTTSHFSVLSFTPRODHDDLTCHVDFSRK 222	A, Experimental source: clone p18236 A, Note: the authors translated the codon CAG for residue 350 as Asn
4 CPPLRPLITWTGTEELLDPIGKERIEDDLGSKSLLGSLRFRPRKEDLGRRVGCGVTFINS 223	Kibloom, Fish Battenberg, E.L.F.; Miller, K.U.; Sulcille, U.S. J. Neurosci. 5, 1781-1802, 1985 A;Title: Immunocytochemical mapping of 1B236, a brain-specific neuronal polypeptide deduc
223 GVGAQRTVRLRVAYAPRDLVISISRDNTPDP 253	A;Reference number: I56564; MUID:85263773; PMID:4020419 A;Accession: I56564; translated from GB/EMBL/DDBJ A:Status: preliminary: translated from GB/EMBL/DDBJ
4 PENLROMVSQANRTULEN	A;Molecule_type: mRNA A;Residues: 'KS' 311-626 <res> a.chose_reference: GR.W16702: NID:G203181: PIDN:AAA40R31.1: PID:G203182</res>
GRNLRLLLSNVGPDDGG8FSCVAENRHGRHNRSLQLRVAYAPRAPVING-SLWVVSGDPV 342	R, Sutcliffe, J.G.; Milner, R.J.; Bloom, F.B. Cold Spring Harb. Symp. Quant. Biol. 48, 477-484, 1983
287 CLVCVTHSSPPARLSWTQRCQVLSPSQPSDFGVLELPRVQVEHBGEFTCHARHPLGSQHV 346 :	A;Title: Cellular localization and function of the professis encoded by Drain-specific mkr. A;Reference number: IS2892; MUID:84206577; PMID:6586369 A;Accession: IS2892; MuiD:84206577; PMID:6586369
347 SLSLSVHYKKGLI	A;Status: prefilminary; transfaced from GD/EMBJ/DBDG A;Molecule type: mRNA A;Residues: 'KS',311-626 <re2> A:Cross-references: CR-M11721: NTD:G206780: PIDN:AAA42082.1: PID:G206781</re2>
SNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRH	C;Comment: The sequence contains five presumably extracellular domains that are distantly C;Comment: The long form predominates in early postnatal life; alternative splicing produ C;Comment: The papers cited variously predict the mature protein to begin at residue 17,
463 PPGSDGSITGI-LTLRGPLEPRLLVLCAARNKHGTTARQLRFHHPGGLVWAK 513	C, Genetics:

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Molecule type: mRNA
Residues: 565-582 <TRO>
                                     A;Molecule type: mRNA
A;Residues: 1-582 <LAI>
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                                 Superfamily: myelin-associated glycoprotein; immunoglobulin homology
Keywords: alternative splicing; brain; cell adhesion; duplication; glycoprotein; trans
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Nielternate names: 18236; brain neuron cytoplasmic protein 3; MAG
Caspecies: Rattus norvegicus (Norway rat)
Caspecies: 2011-1990 #sequence revision 30-Jun-1990 #text_change 16-Jun-2000
Caspeciession: 829028; B27185; A60055
Caspecession: 829028; B27185; A60055
Caspecession: C.; Brow, M.A.; Nave, K.A.; Noronha, A.B.; Quarles, R.H.; Bloom, F.E.; Milner, R.
                                                                                                                                                                                                                                                  P½99,223,246,315,332,406,450,454,Binding site: carbohydrate (Asn) (covalent) #status pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 VIVEMNSSVEAIEGSHVSLLCGADSNPPPLLTWMRDGMVLREAVAESLYLDLEEVTPAED 300
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                                                                                                                                                                                                                                                                                                                                                                                                                  10 FWIMISASRGGHWGAWMPSSISAFEGTCVSIPCRFDFP--DELRPAVVHGVWYFNSPYPK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 KGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFRVERGSYVRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 NYPPVVFKSRTQVVHESFQGRSRLLGDLGLRNCTLLLSTLSPELGGKYYFRGDLGGYNQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 NFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPP--PSFSWTGAALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 GEPTVLGRLREDEGTWVQVSLLHFVPTREANGHRLGCQAAFPNTTLQFEGYASLDVKYPP
                                                                                                                                                                                                                                                                                                                                                                           21 FWIRVQ-------ESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWFKAVTETT
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                                                                                                                                                                                                                                                                                                                                 Indels 173;
                                                                                                                                                                                                                                                                                       10.9%; Score 295.5; DB 1; Length 626; 22.2%; Pred. No. 2e-12; ive 85; Mismatches 239; Indels 173.
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                                                                                                                                                                                                                                                                            July Match 10.5
Dest Local Similarity 22.2
Matches 142; Conservative
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Proc. Natl. Acad. Sci. U.S.A. 84, 4337-4341, 1987
A,Title: Two forms of 18236/myelin-associated glycoprotein, a cell adhesion molecule for A,Reference number: A29028; MUID:87232001; PMID:2438699
A,Accession: B29028
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R;Salzer, J.L.; Holmes, W.P.; Colman, D.R.
J. Gell Biol. 104, 957-965, 1987
A;Title: The amino acid sequences of the myelin-associated glycoproteins: homology.
A;Reference number: A27185; MUID:87166195; PMID:2435742
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A, Residues: 149-582 < SAL>
A, Residues: 149-582 < SAL>
A, Cross-references: GB:X06554; NID:956614; PIDN:CAA29797.1; PID:91334302
R, Tropak, M.B.; Johnson, P.W.; Dunn, R.J.; Roder, J.C.
R, Tropak, M.B. Brain Res. 4, 143-155, 1988
A, Title: Differential splicing of MAG transcripts during CNS and PNS development.
A, Reference number: A60055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 SQGT-----KPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAP 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
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OY 363 FSNGAFLGIGITALLFLCLALIMKILPKRRTQTETPRPRFSRHST1 409 Db 414ILLESHCAAARDTVQCLCVVKSNPEPSVAFELPSRNVTV 453	Db 357 LTIFKEKQILATVIYESQLQLELPAVTPEDDGEYWCVAENQYGQRATAFNLSVEFAP 413 Qy 360 STAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTI 409
RESULT 7 B33765 myelin-associated glycoprotein - mouse myelin-associated glycoprotein - mouse C; Species: Mus musculus (house mouse) C; Species: Musculus (house mouse) C; Species: Musculus (house mouse) C; Steession: B33785; S05687; S02774 B; Pujita, N.; Sato, S.; Kurihara, T.; Kuwano, R.; Sakimura, K.; Inuzuka, T.; Takahashi, Biochem. Biophys. Res. Commun. 165, 1162-1169, 1989 A; Title: cDNA cloning of mouse myelin-associated glycoprotein: a novel alternative splic A; Reference number: A33785, WUID:90121220; PMID:2482022 A; Status: preliminary A; Molecule: 1-637 < FUU.> A; Residues: 1-637 < FUU.> A; Accession: A33785 A; Status: preliminary A; Accession: A33785 A; Status: preliminary A; Accession: A33785	Pb 414IILLESHCAAARDTVQCLCVVKSNPEPSVAFELPSRNVTV 453 RESULT 8 S50065 sialoadhesin - mouse C;Species: Mus musculus (house mouse) C;Date: O'-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004 C;Accession: S50065 R;Crocker, P.R: Mucklow, S:; Bouckson, V.; McWilliam, A.; Willis, A.C.; Gordon, S.; Milc EMBO J. 13, 4490-4503, 1994 A;Title: Sialoadhesin, a macrophage sialic acid binding receptor for haemopoietic cells v A;Reference number: S50065; MUD:95009950; PMID:7925291 A;Accession: S50065 A;Retus: preliminary A;Molecule type: mRNA A;Residues: 1-1694 <cro. a;cross-references:="" embl:236293;="" nid:g557253;="" pid:g55725<="" pidn:caa85290.1;="" td="" uniprot:062230;=""></cro.>
A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 1-582 cFU3. A; Residues: 1-582 cFU3. A; Cross-references: GB:M31811; NID:g199016; PIDN:AAA39487.1; PID:g199017 A; Cross-references: GB:M31811; NID:g199016; PIDN:AAA39487.1; PID:g199017 B; Fujita, N.; Sato, S.; Kurihara, T.; Inuzuka, T.; Takahashi, Y.; Miyatake, T. FEBS Lett. 232, 323-327, 1988 A; Tetle: Developmentally regulated alternative splicing of brain myelin-associated glycc A; Reference number: S02374; MUID:88242820; PMID:2454205 A; Accession: S02374 A; Molecule type: mRNA A; Residues: 310-374; S66-573, 584-588 cFU2. A; Accession: S02374 A; Molecule type: mRNA A; Residues: 310-374; S66-582 cFU4.	Query Match Best Local Similarity 25.7%; Pred. No. 1.8e-08; Matches 107; Conservative 52; Mismatches 179; Indels 78; Gaps 14; Qy 5 LLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRODWTGSTPAVGYWFRAV 64
Cigenetics: A;Map position: 7 C;Genetics: A;Map position: 7 C;Superfamily: myelin-associated glycoprotein; immunoglobulin homology C;Keywords: alternative splicing; glycoprotein; transmembrane protein C;Keywords: alternative splicing; glycoprotein; transmembrane protein F;152-19/Domain: immunoglobulin homology <imm2> C;Ceywords: alternative protein F;152-Natch Bost Local Similarity 23.1%; Pred. No. 6e-12; Matches 110; Conservative 62; Mismatches 184; Indels 121; Gaps 14;</imm2>	Db 122 SNRWLDVK-ĞTTVTVŤTDPSPPTITIPEELREĠMSRNFNĊSTPYLCLĢEKQVŠLQWRĠQD 180 Qy 183AALSSQGTKPTTS-HFSVLSFTPRPQDHDTLTCHVDFSRKGVSAQRTVRLRVAYA 237 Db 181 PTHSVTSSFQSLEPTGSYHQTTLHMALSWQDHGRTLLCQFSLGAHŠSRKEVYLQVPHA 238 Qy 238 PRDLVISISRDNTPDPPRNLRVWVSQANRTVLENLG
	Qy 274NGTSLPVLEGQSLCLVCVTHSSPPAR 299 Db 299 NDSGAYTCQATNDMGSLVSSPLSLHVFMAEVRANPAGPVLENETVTLLCSTPKEAPQELR 358 Qy 300 LSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSGHVS-LSLSVHY 354
OY 129 NEMNDGFPLKVTALTOKPDVYIPETLEPGOPVTVICVFNWAFEECPPPSFSWTGAALS 186 128 TESEHSVLDIVNTPNIVVPPEVVAGTEVEVSCAVPDNCPELRPELSWLGHEGL 180 QY 187 SQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAXAP 238 181 GFTVLGRLREDGTWVQVSLLHFVPTREANGHRLGCAAFPNTTLQFEGYASLDVKYPP 240 QY 239 RDLVISIS	RESULT 9 149583 differentiation antigen - mouse CiSpecies: Mus musculus (house mouse) CiDecies: 02-011-1996 #sequence_revision 02-011-1996 #text_change 09-011-2004 CiDecies: 02-011-1996 #sequence_revision 02-011-1996 #text_change 09-011-2004 CiDecies: 02-011-19983 Rilaw, CiDecies: 02-011-19983 A;Ittle: Organization of the murine Cd22 locus. Mapping to chromosome 7 and characterizat A;Reference number: 149583; MUID:93315834; PMID:8100843 A;Reference number: 149583; MUID:93315834; PMID:8100843 A;Retus: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mINA A;Molecule type: mINA A;Ross-references: UNIPPOT:P35329; GB:L16928; NID:g348965; PIDN:AAA02562.1; PID:g348966 C;Genetics: A;Gene: CD22

Db 213 NVYTESKLTPQPKWTDHGKSVKCQVQHSSK-VLSECTVHLDVKYTPKLEIKVNPTEVEKN 271 Qy 239RDLVISISRDNTPDPFNIRVWVSQANRTVL	ABSULT 11 C. Secies 1 Gmo as appens (man) C. Species: Home asplens (man) C. Species: Home asplens (man) C. Accession: A35649 R. Stamenkovic, 1.; Seed, B. R. Stamenkovic, 1.; Seed, B. Nature 345, 74-77, 1990 A.Title: The B-cell antigen CD22 mediates monocyte and erythrocyte adhesion. A, Reference number: A35648; MUD: 90231465; PMID: 1691828 A, Accession: A35648 A, Molecule type: mRNA A, Residues: 1-647 <sta> A, Residues: 1-647 <sta> A, Cross-references: GB: X52785; NID: 929778; PIDN: CAA36988.1; PID: 929779 C, Genetics: A, Accession: A600-condender: A170-condender: A170-condende</sta></sta>	ve splicing; B-cell; cell adhesion; dimer; glycoprotei sequence #status predicted <sig> sequence #status predicted <sig> sequence #status predicted <sig> unoglobulin homology <iwm> nsmembrane #status predicted <twm> rescellular #status predicted <twm> 7.6%; Score 206.5; DB 2; Length 647; ty 19.0%; Pred: No. 2.2e-06; ervative 87; Mismatches 212; Indels 257; Gaps SSLLGGSQAMDGREWI-RVQESVMVPEGLGISVPCSFSYPRQ </twm></twm></iwm></sig></sig></sig>	Oy 19 DWGSTPATGYWFAATTINGAPVAINHOSREVEMSTRCHCALGUIGHT 108 63 EYNKNISKED-GTRLYESTKOGKVPSEQKRVQFLGDKNK-NCTLSIHPV 109 CY 109 QWQDESQYFFRVERGSYVRYNFWNDGFFLKVTALTQKPDVYIPETLEPEQGPVTVICVFN-167 110 HLNDSGOLGLRMESKTEKWMERIHLNVSERPPPHIQLPPEIQESQEVTLTCKLNF 165 CY 168WAFEGCPPSFSWTGAALSSQGTKPTTSHFSVLSFTRPPQDH 209 166 SCYGYPIQLOWLLEGVPWRQAAVTSTSLTIKSVPTRSELKFSPQWSHIGKI-VTCQLQDA 224 CY 210 D	Db 225 bGKFLSNDTVQLNVKHPPKKVTTVIQNPMPIREGDTVTLSCNYNSSNPSVTRYBWKPHGA 284 Qy 225 241 Db 285 WEEPSLGVLKIQNVGWDNTTIACAACNSWCSWASPVALNVQYAPRDVRVRKIKPLSEIHS 344
Query Match Beat Local Similarity 21.7%; Pred. No. 1.3e-07; Beat Local Similarity 21.7%; Pred. No. 1.3e-07; Matches 97; Conservative 64; Mismatches 188; Indels 98; Gaps 5 LLLSSILGGSQAMDGRPW-IRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWF	DD 229 TVRLRVAYAPETTESVTSSIKNVYTESKLTFOPKWIDHGKSVKCQVOHSSE-VLSER 241 229 TVRLRVAYAPETTELEIKVNPTEVEKUNSVTMTCRVNSSNPKLRTVASVMFKDGREDGELE 301 229 VAVSQANRTVL	SULT 10 51.2 22 homolog/B lymphocyte-restricted adhes 22 homolog/B lymphocyte-restricted adhes 22 homolog/B lymphocyte-restricted adhes 23 homes: Ms. Ms. Law. C.L.; Santos-revision 10- Accession: A46512 Fitle: Identification and characterizati Reference number: A46512; MUID:93017867; Accession: A46512 Status: preliminary; not compared with colecule type: mulleic acid Residues: 1-868 crCR> Experimental source: B cell lymphoma 38C	A;Note: sequence extracted from NCBI backbone (NCBIP:116156) Query Match Best Local Similarity 21.7%; Pred: No. 3.6e-07; Matches 92; Conservative 57; Mismatches 173; Indels 101; Gaps 15; Qy 33 EGCISVPCSFS-YPRODWTGSTBAYGYWFRAVTETTKGAPVATNHQSREVEMS 85	146 PDVYIPETLEPGQPVTVICVPNWAFBECPPSFSWTGAALSSQGTKPTT 194

oy Db	242VISISRDNTPDPPBNLRVMVSQANTTULENL 272	ò a	49 DWTGSTPAYGYWFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDA 108
Oy Dp	273 GNGTSLPVL	ò a	109 QWQDESQYFFRVERGSYVRXNFWNDGFFLKVTALTQKPDVY1PETLEBGQPVTVICVEN- 167
Qy Db	312 SQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLS-LSVHYKKGLISTAFSNGAFLG 370	ð 8	168WAFBECPPSFSWTGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHV 217
ζλ Dp	371 IGITALLFLCLALIIMKILPKRRTQTETPRFRFSRHSTILDYINVVPTAGPLAQ 424	ò q	218 -DFSRKGUSAQRTVRLRVAVAPRDLVISISRDNTPDPPE 255
oy en	425 KRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPESQESQEELHYAT 484	ζο qq	256
Qy Dp	485 INFPGVR.PRPEARMPKGTQADYAEVK 510	දු දු	278LPVLEGGSLCLVCVTHSSP-PARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEF 333 338 ILHSPAVEGSQVEFLCMSLANPLPTNYTWYHNGKEMQGRTEEKVHIPKILPWHAGTY 394
RESULT 1 JH0371	12 adheatar mootate Onto here enline form moonirear - himan	oy Db	334 TCHARHPLGSOHVSLSLSVHYKKGLISTAFSNGAFLGIGITALL 377
N, Altern C, Specie C, Date:	nate names: B-cell membrane protein CD22 38-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004 130-387-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004	RESULT A32164 biliam	r 13 ry olycoprotein 1 precursor, splice form a - human
R, Wilson J. Exp.	J. G.L.; Fox, C.H.; Fauci, A.S.; Kehrl, J.H. Med. 173, 137-146, 1991 Annual Transfer of the Boot Mediator of B.B cell intera	N, Con	sinate names: transmembrane carcinoembryonic antigen 1 (TM1-CEA); transmembrane carcains bllary glycoprotein 1, splice form b; biliary glycoprotein 1, splice form x is s. Homo saniens (man)
A; Refere A; Access A; Molecu		C,Dat C,Acc R,Hin	C.Date: 20-Apr-2000 #sequence revision 20-Apr-2000 #text_change 09-Jul-2004 C.Accession: A32164; A30127; B30127; A48078; S45664; S65939; A30847; G44476 R.Hinoda, Y.Y. Neumaler, M.; Hefta, S.A.; Dzreniek, Z.; Wagener, C.; Shively, L.; Hefta, I
A; Residu A; Cross- A; Experi	des: 1-847 <mili> -references: UNIPROT:060926; GB:X59350; NID:g36090; PIDN:CAA42006.1; PID:g36091 mental source: B lymphocyte</mili>	A,Ref A,Ref A,Gon A,Ago	FIOC. Nati. Acad. Sci. 00, 100, 100, 100, 100, 100, 100, 100,
R;Wilson J. Immun	n, G.L.; Najfeld, V.; Kozlow, E.; Menniger, J.; Ward, D.; Kehrl, J.H.	A; Wol	A;Molecule type: mRNA A;Molecule type: mRNA A;Molecule type: mRDA A;Molecule type: mRDPOT: b13688. GB:T01868. NTD:G179439. PTDN:AAA51826.1: PTD:G179440
A;Title: A;Refere A;Access	: Genomic structure and chromosomal mapping of the numan CD22 gene. ance number: 156171; MUID:93267103; PMID:8496602 lion: 156171	A;Cro R;Hin Proc.	Aj.Coss-retenuces: Unirolitascoop, Os.co.soop, Nr. 31.735, Filmoda, Y.; Neumajer, M.; Hefta, S.A.; Dzzeniek, Z.; Wagener, C.; Shively, L.; Hefta, I. Proc. Natl. Acad. Sci. U.S.A. 85, 6959-6963, 1988
A;Status A;Molecu A:Residu		A,Tit A,Ref A,Con	le: Molecular cloning of a cDNA coding biliary glycoprotein I: Primary structure of srence unuber: A94206; MUID:88320555; PMID:2457922 Cents: annotation
A, Cross-C, Geneti		A, Not R, Bar	e: the sequence shown in this reference has been completely corrected in reference i nett, "R.; Kretschmer, A.; Austen, D.A.; Goebel, S.J.; Hart, J.T.; Elting, J.J.; Ki is st. 1 no 257-276. 1989
A; Gene: A; Cross- A; Map po		A;Tit A;Ref A;Acc	11 Carcinoembryonic antigens: alternative splicing accounts for the multiple mRNAs erence number: A22752; MUID:89139550; PMID:2537311 ession: A30127
C; Keywor F;1-19/E F;20-847 F;346-39	C. Keywords: alternative splicing; B-cell; cell adhesion; dimer; glycoprotein; phosphopro F;1-19/Domain: signal sequence #status predicted <sig> F;20-847/Product: B lymphocyte cell adhesion protein #status predicted <mat> F;346-398/Domain: immunoglobulin homology <imm1></imm1></mat></sig>	A; Mol A; Res A; Cro A; Exp	A;Molecule type: mRNA A;Residues: 1-526 <bar1> A;Cross.references: EMBL:X16354; NID:g37197; PIDN:CAA34404.1; PID:g37198; EMBL:X14784 A;Experimental source: splice form a</bar1>
F;688-70 F;67,101 F;764,78	(coval	A; Res	GCOLECTOR RNA idues: 1-319,'D',417-526 (BAR2) ss-references: BMBL:X14831; NDD(337199; PIDN:CAA32940.1; PID:g37200; EMBL:X14784 primantal cource: solice form b
Query Match Best Local Matches 9	7.5%; Score 202.5; DB 2; Length 847; Similarity 21.0%; Pred. No. 5.7e-06; 8; Conservative 69; Mismatches 182; Indels 117; Gaps 19;	R;Bar Mol. A;Tit	nett, T.R.; Drake, L.; Pickle II, W. Cell. Biol. 13, 1273-1282, 1993 le: Human biliary glycoprotein gene: characterization of a family of novel alternati Prence number: A48078; WUID:93140765; PMID:8423792
Sy Dp	1 MLEPLISSLIGGSQAMDGRFWI-RVQESVWVPEGLCISVPCSFSYPRQ 48 : :	A, ACC A, Mol A, Res A, Cro	A,Accession: A48078 A,Molacule V.pe: mNA A,Residues: 124-141,'H',417-526 <bar3> A,Residues: 124-141,'H',476742; NID:g179480; PIDN:AAA57142.1; PID:g179481</bar3>

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A; Introns: 18/1; 53/3; 118/1; 139/3; 169/1; 229/1; 272/3; 320/1; 329/1; 371/2
C; Superfamily: advanced glycosylation end products receptor; immunoglobulin homology: C; Keywords: receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: T09062
R; Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.B.; Dankers, C.; Lasky, S.; Loretz, S.; Submitted to the EMBL Data Library, October 1997
A; Description: Sequence of the mouse major histocompatibility locus class III regions A; Reference number: 216543
A; Accession: T09062
                                                                                                                                                                                  303 NSVTGCNRTTV-----KTIIVTELSPVVAKPQIKASKTTVTGDKDSVNLT-----CST 350
                                                                                                                                                                                                                                                                              421
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    248 YYRPGANLSLSCYAASNPPAQYSWLINGTFQQSTQE-----LFIPNITVNNSGSYTCHAN 302
                                                                                       --- NGAFLGIGITALLFLCLA 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         369 LGIGITALLFLCLALIIMKILPKRRIQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQ 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 NGSLLLPATGIVDEGTFRCRATNRRGKEVKSNYR----VRVYQIPGKPEIVDPASELTA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --PTTSHFSVLS-F 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 SVPNKVGTCVSEGSY---PAGTLSWHLDGKLLIPDGKETLVKEETRRHPETGLFTLRSEL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203 TPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVISISRDNTPDPPENLRVMVS 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --KKGLISTAFSNGAF 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           287 PEVGHEDEGTYSCVATHPSHGPQESPPVSIRVTETGDEGPAEGSVGESGLGTLALALGIL 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 12402 <ROW>
A;Cross-references: UNIPROT:035444; EMBL:AF030001; NID:g2564945; PID:g2564950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Mus musculus (house mouse)
C;Species: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                        .---TAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    410 IMLNVNYNALPQ--ENGLSPGAIAGIVIGVVALVALIAVALACFLHFGKTGRASDQRDLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             468 BHK------PSVSNHTQDHSNDPPNXMNEVTYSTLNFBAQQPTQPTSASPSLTATEIIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OKKOYQLPSFPEPKSSTQ--APESQESQEELHYATLNFPGVRP-RPEARMPK--GTQADY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVIPTQGGTHPTFSCSFS-LGLPRRRPLNT----APIQL-----RVREPGPPEGIQLLVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      263 QANRIVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 PEGGI------VAPGGTVTLTCAISAQPPPQVHWIKDGAPL-PLAPSP--VLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable advanced glycosylation end-products receptor precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.8%; Score 184; DB 2; Length 402;
larity 23.4%; Pred. No. 4.1e-05;
Conservative 46; Mismatches 139; Indels 1.
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                                                                                                                                                                                                                                                                              383 L---IIMKILPKRRTQTETPRPRFSRHSTILDYINVVP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              323 PRVQVEHEGEFTCHARHPLGSQHVSLSLSVHY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;31-100/Domain: immunoglobulin homology < IMM>
                                                                                                HPL-GSQHVSLSLSVHYKKGLISTAFS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                            422 LAOKRNOKATPNSPRTPLPPGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              507 AEVKFQ 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 101; Conserv
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Casuperfamily: carcinomehryonic antigen, carcinoembryonic antigen precursor amino-termin (Casuperfamily: carcinomehryonic antigen; surface antigen; transmembrane protein (Casuperfamily: carcinomehryonic antigen precursor amino-terminal homology «CEAN»

P:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology «CEAN»

P:1-34/Domain: signal sequence #status predicted «SIG»

F:1-35-6/Domain: signal sequence #status predicted «SIG»

F:35-428/Domain: extracellular #status predicted «EXT»

F:35-141, 'H',417-526/Product: biliary glycoprotein 1, splice form x #status predicted «ME, 15-140, "H',417-526/Product: biliary glycoprotein 1, splice form x #status predicted «ME, 15-140, "MI)

F:160-217/Domain: immunoglobulin homology «IMM:)

F:25-301/Domain: immunoglobulin homology «IMM:)

F:25-301/Domain: immunoglobulin homology «IMM:)
                                                                                                                                                                                                                                                                                                                                                                                                  Molecule type: DNA
Residues: 1-21 <HAU>
Residues: 1-21 <HAU>
References: EMBL:X67277, NID:g29447; PIDN:CAA47694.1; PID:g606777
Negellec, P.; Turbide, C.; Beauchemin, N.
T. Biochem. 231, 104-114, 1995
Title: Characterization and transcriptional activity of the mouse biliary glycoprotein
Reference number: 865939; MUID:99354678; PMID:7628460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Experimental source: splice form x winder in the complete translation are shown to sequence extracted from NCBI backbone (NCBIN:123602, NCBIP:123606)
Whote: neither the complete nucleic acid sequence nor the complete translation are shown to complete the complete nucleic acid sequence nor the complete translation are shown to be shown to a sequence in 1994 and the complete translation in the complete sequence of the number of the nu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Action, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstroem, S. enomics 14, 384-390, 1992

"Title: Identification of three new genes and estimation of the size of the carcinoembra Reference number: A44476; WIID:93052339; PMID:1427854

"Conference annotation; alignment of related sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mikesidues: 1-21 (NED)
Mytross-references: EMBL:X67277; NID:g29447; PIDN:CAA47694.1; PID:g606777
Mytross-references: EMBL:X6727; NID:g29447; PIDN:CAA47694.1; PID:g606777
Mytros: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 GYSWYKG--ERVDG-----NRQIVGYAIGTQQATPGPANSGRETIYPNASILIQNVT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 MQDESQYFFRVERGSYVRYNFWNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 -PELPKPS-----ISSNNSNPVEDKDAV-AFTCEPETQDTTYLWWINNQSLPVSP--- 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 FEECPPPSFSWTGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----GOSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGERFTCHAR 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LILISSLIGGSQAMDGRFWIRVQESVMVPEGLCISVP-----CSFSYPRQDWTGSTPAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 196;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.9%; Score 186; DB 1;
llarity 21.5%; Pred. No. 4.2e-05;
Conservative 80; Mismatches 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tatus: preliminary; translation not shown
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Best Local Similarity
Matches 130; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type: DNA
Residues: 1-21 <NED>
                                                                                                                                                                                                                                                                                                                          Accession: S45664
Status: preliminary
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LRWFKEĠĠQLPPCHSVQDĠVLRIQNLDQSCQĠTYIĊQAHGPWGKAQAŚAQLVIQALPSVL 3490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3172 ISSAKPSDAGTYVCLAQNALGTAQKQVEVIVDTGAMAPGAPQVQAEEAELTVEAGHTATL 3231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3337 SSLPGR--ATARNELLHFERAAPEDSGRYRCRV--TNKVGSAEAFAQLLVQGPPGSLPAT 3392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SISRDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLE----GOSLCLVCVTHSSPPAR 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 ISSOGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDL-VI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.7%; Score 180; DB 2; Length 4391;
20.4%; Pred. No. 0.0015;
.ive 68; Mismatches 214; Indels 222;
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Best Local Similarity 20.4
Matches 129; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                               parlecan precursor - human

NyAlternate names: basement membrane heparan sulfate proteoglycan; heparan sulfate prote
C;Species: Homo sapiens (man)
C;Date: 07-Apr-1994 #sequence revision 07-Apr-1994 #text change 12-Jul-2004
C;Accession: A38096; S19256; S77946; A41059; A40306; B33525; A33625; A41736
R;Murdoch, A. D.; Dodge, G.R.; Cohen, I.; Tuan, R.S.; Iozzo, R.V.
C;Accession: A38096; S19256; S77946; A41059; A40306; B33525; A33625; A41736
R;Mittle: Primary structure of the human heparan sulfate proteoglycan from basement membr
cor, laminin, neural cell adhesion molecules, and epidermal growth factor.
A;Reference number: A38096
A;Molecule type: mRWA
A;Residues: 1-4391 <AWNA
A;Residues: 1-4391 <AWNA
A;Residues: 1-4391 <AWNA
A;Residues: 1-1050 CB:M85289; NID:g184426; PIDN:AAA52700.1; PID:g184427
R;Kallunki, P.; Tryggvason, K.
J. Cell Biol. 116, 559-571, 1992
A;Title: Human basement membrane heparan sulfate proteoglycan core protein: a 467-kD proference number: A41736; MUID:92112994; PMID:1730768
A;Molecule type: mRNA
A;Residues: 1-57, D', S9-434, A', 436, FL', 438-449, 'Q', 451-502, 'A', 503-792, 'K', 794-908, 'R'
A;Title: Human basement membrane heparan sulfate proteoglycan core protein: a 467-kD proference number: A41736; MUID:92112994; PMID:1730768
A;Molecule type: mRNA
A;Ressidues: 1-57, D', S9-434, 'A', 436, 'FL', 438-449, 'Q', 451-502, 'A', 503-792, 'K', 794-908, 'R'
A;Title: Human basement membrane heparan aulfate after a farmat a farmat a farmat basement and a farmat a farmat basement and a farmat a farmat basement and a farmat a farmat basement a farmat basement and a farmat 
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A. Reference number: R. S79469
A. Reference number: R. S79469
A. Reference number: R. L. Byers, M. G., Restilae, M.; Shows, T. B.; Tryggvason, K. Genomics 11, 389-396, 1991
A. Rititle: Cloning of human heparan sulfate proteoglycan core protein, assignment of the galacter number: A41059; MuID:92120660; PMID:1685141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 'RT', 892-908,'R', 910-1101,'L',1103-1132,'L',1134-1221,'L',1223-1397 < KA2>
A; Residues: 'RT', 892-908,'R', 910-1101,'L', 1103-1132,'L',1134-1221,'L',1223-1397 < KA2>
A; Cross-references: GB: 876436; NID: 9243370; PIDN: AABZ1121.1; PID: 9243371
R; Dodge, G.R.; Kovalszky, I; Chu, M.L.; Hassell, J.R.; McBride, O.W.; Yi, H.F.; Iozzo,
Genomics 10, 673-680, 1991
A; Title: Heparan sulfate proteoglycan of human colon: partial molecular cloning, cellula
A; Reference number: A40306; MUID: 91365376; PMID: 1679749
A; Residues: 1018-1405, 'G', 1407-1409, 'G', 1411-1465 < DOD>
A; Residues: 1018-1405, 'G', 1407-1409, 'G', 1411-1465 < DOD>
A; Residues: Schuerences: GB: M64283; NID: 9184424; PIDN: AAAS2699.1; PID: 9184425
A; Cross-references: Chuerences: Chueren, B.; De Cock, B.; Paulsson, M.; Cassiman, J.J.; van der
J. Cell Biol. 109, 3199-3211, 1989
A; Title: Matrix-associated heparan sulfate proteoglycan: core protein-specific monoclona
365
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                                                               429 KATPNSPRTPLPPGAPSPESKKNOKKOYOLPSFPEPKSSTQAPESQESQEELHYATLNFP
                                                                                                                     ---APESQEDEEE--RAELN--
--VGAILWRKRO
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A,Molacule type: protein
A,Residues: 1379-1334, X',1386-1388, X',1390-1398 <HE2>
A,Accession: A33625
A,Accession: Cype: protein
A,Molacule type: protein
A,Residues: 2166-2171, X', 2173-2175, X',2177-2185 <HE3>
A,Note: peptide potentially matches four different regions of
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November 5, 2004, 13:50:17; Search time 59.6073 Seconds (without alignments) 3081.324 Million cell updates/sec
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1 MLPLLLSSLLGGSQAMDGR.....RPEARMPKGTQADYAEVKFQ 512
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(c) 1993 - 2004 Compugen Ltd.
                                                                                   OM protein - protein search, using sw model
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2002273 Total number of hits satisfying chosen parameters: 2002273 segs, 358729299 residues BLOSUM62 Gapop 10.0 , Gapext Searched:

Scoring table:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_23Sep04:*
1: geneseqp1980s.*
2: new_ geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1990s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	00100880020408140808140844408888908888498848	Abo02747 Human sec Abr74901 Human sec
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Abr94663 Human sec	Novel	Abu85636 Human PRO	Novel	1 Novel	Abu91717 Novel hum	2 Novel	Abu89410 Human PRO	1 Human	Human	Abu80492 Human PRO	Abr99410 Human sec	Abr98800 Human sec	Abo16323 Human sec	Abr92223 Human sec	Abol8864 Human sec	Abr78285 Human sec	Abu85021 Novel hum	Abo00160 Novel hum	Aboll492 Human sec
ABR94663	: AB025226	ABU85636	ABU98796	ABU98011		; ABU72232	ABU89410	. ABU86251	. ABU67464		ABR99410	. ABR98800	; ABO16323	; ABR92223	, AB018864	3 ABR78285	3 ABU85021	3 ABO00160	3 ABO11492
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26	27	28			31	32	33	34	35	36	37	38	6 E	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

Human obesity protein binding protein-2 homologue; hOB-BP2h; obesity; obesity, related disorder; therapy. Human obesity protein binding protein-2 homologue #1. AAY97542 standard; protein; 512 AA (first entry) 12-FEB-2001 AAY97542; AAY97542

Homo sapiens.

WO200059942-A2. 12-OCT-2000.

22-MAR-2000; 2000WO-US006682

02-APR-1999; 99US-0127667P

(ELIL) LILLY & CO ELI.

Wei J; Su EW, WPI; 2000-664992/64. N-PSDB; AAA37847 New human obesity protein binding protein-2 homologue nucleic acids, polynucleotides and polypeptides useful for producing medicament for treating obesity and/or obesity-related disorders.

Claim 9; Page 86-88; 92pp; English.

This sequence is a human obesity protein binding protein-2 homologue (hOB-BP2h) of the invention. The hOB-BP2h nucleic acids and polypeptides may be used for the manufacture of a medicament for the treatment of obesity and/or obesity-related disorders. The hOB-BP2h nucleic acids are useful as probes or amplification primers in the detection, quantification or isolation of gene sequences or transcripts, for recombinant expression of hOB-BP2h polypeptides, as immunogens in the preparation and screening of antibodies, and in sense or antisense suppression of one or more hOB-BP2h genes or nucleic acids, host cell or tissue in vivo or in vitro. Antigenic epitope-bearing peptides and polypeptides are useful for raising or screening antibodies that specifically binds to the hOB-BP2h polypeptides.

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Gaps

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Length 512;

120

9

180 240 300

360

420

480

180

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FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
                                                                                                                       1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
                                                                                                                                                         PKAVTETTKGAPVATNHQSREVEMSTRGRPQLTGDPAKGNCSLVIRDAQMQDESQYFPRV
                                                                                                                                                                                                                       ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW
                                                                                                                                                                                                                                                  121 ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW
                                                                                                                                                                                                                                                                                    TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
                                                                                                                                                                                                                                                                                                             181 IGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
                                                                                                                                                                                                                                                                                                                                                  LVISISRDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARL
                                                                                                                                                                                                                                                                                                                                                                                 241 LVISISRDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARL
                                                                                                                                                                                                                                                                                                                                                                                                               SWIQRGQVLSPSQPSDPGVLELPRVQVBHEGEFTCHARHPLGSQHVSLSLSVHYKKGLIS
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                                                                                           1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immune system disease; leukaēmia; allergy; inflammatory disease;
tissue damage; allergic rhinitis; osteoarthritis; Crohn's disease;
psoriasis; rheumatoid arthritis; conjunctivitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sialic acid-binding Ig-related lectin, Siglec-BMS-L3-995-3
                            . Score 2706; DB 3;
. Pred. No. 2.8e-205;
0; Mismatches 0;
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ilarity 100.0%;
Conservative 0;
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                                     gwery match
Best Local Similarity
Matches 512, Conserv
Sequence 512 AA;
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                              Query Match
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The invention relates to an isolated SIGIBC (sialic acid-binding Igrelated lectin) protein (1). Pharmaceutical compositions comprising (1) are useful for treating immune system diseases such as asthma, lenkaemia or other allergic or inflammatory diseases. Extracellular domains of (1) represent potential markers for screening, diagnosis, prognosis, follow or other allergic or inflammatory diseases. Extracellular domains of (1) is useful as a target for drugs which inhibit inflammation, tissue damage and remodeling in asthma, and indeping methods. (1) is useful as a target for drugs which inhibit inflammatory diseases such as allergic rhinitis, osteoarthritis, crohn's disease, psoriasis, rheumatorid arthritis, conjunctivitis, etc. (1) is also useful for menitoring the course of disease or disorders, and for identifying agents that bind with and/or modulate the biological activity of SIGIEC-BMS proteins. The nucleic acid molecules (11) are useful in diagnosis and/or prognosis methods, and to detect the presence and/or amount of SIGIEC-BMS nucleotide sequences and/or SIGIEC-BMS copy number is determined for detecting diseases or disorders associated with SIGIEC-BMS transcripts or proteins. The SIGIEC-BMS transcripts or proteins.

The SIGIEC-BMS proteins and in diagnostic imaging technology.

ANURTON ANURTON SUPPLIES THOUGHS are also used to detect, sort or isolate cells expressing SIGIEC-BMS proteins and in diagnostic imaging technology.
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                                                                              Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein molecules useful for treating immune system diseases such as asthma, leukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERGSYVRYNPMNDGFFLKVTALTOKPDVYIPETLEPGOPVTVICVFNWAFEECPPPSFSW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.4%; Score 2580.5; DB 5; Length 697; 73.2%; Pred. No. 3.6e-195; cive 1; Mismatches 1; Indels 185;
                                                                                                                                                                        Example 11; Fig 6; 209pp; English
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Matches 510; Conservative
                  WPI; 2002-241565/29.
N-PSDB; ABK43373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 697 AA;
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355

Whitney G;

Chang H,

Longphre M,

(BRIM) BRISTOL-MYERS SQUIBB CO.

20-JUL-2001; 2001WO-US023082

31-JAN-2002

21-JUL-2000;

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The invention relates to an isolated nucleic molecule that is at least 95% identical to 18 human cDNA sequences representing 12 novel genes encoding secreted proteins or a polynucleotide fragment of the cDNA sequence contained in American Type Culture Collection (ATCC) deposit No. defined in the specification, its species homologue, a variant or allelic
                        415
                                                                          475
                                                900
                                                                                                  99
ELLEGNSSODSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAOSGSILQLPDK 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human secreted nucleic acid molecules and polypeptides, useful for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation, immune disorders, neurological and blood clotting
                                                                                        KGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINV
                                           KGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRFRFSRHSTILDYINV
                                                                        VPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPESQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Greene JM;
                                                                                                                                                                                                                                                                                                                 cytostatic; antiinflammatory; immunomodulator; neuroprotective; hemostatic; gene therapy; cancer; inflammation; immune disorder; neurological disorder; blood clotting disorder; food additive; preservative; human; secreted protein.
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                                                                                                                                                                                                                                                                                          novel secreted protein from cDNA HDPCL05
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                                                                                                                                                                                                                ADA27153 standard; protein; 697
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27-CCT-1999; 99WO-US025031.
19-APR-2000; 2000US-0194792P.
30-CCT-2000; 2000US-0243792P.
18-APR-2001; 2001US-00836353.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-OCT-2001; 2001US-00984130
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Crocker P
                                                                                                                                                                                                                                                                  (first entry)
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N-PSDB; ADA27152.
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KENNY J J.
OLSEN H S.
MOORE P A.
WEI Y.
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M, Liu D,
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CROCKER 1
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                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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(GREE/)
(RUBE/)
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the polynucleotide having a polynucleotide capable of does not hybridising under conditions the polynucleotide, where the polynucleotide does not hybridise under stringent conditions to a nucleic acid molecule constraint and a nucleotide sequence of only A or residues. Also included are recombinant vectors, host cells (for producing the polypeptide), the secreted polypeptide (comprising a sequence that is at least 95% identical to a polypeptide fragment, domain, epitope, full-length protein, variant, allelic variant or species homologue), antibodies that specifically bind to the polypeptides, diagnosing, treating, preventing or amelicating a medical condition by administering the polynucleotide or the polypeptide, the gene corresponding to the cDNA sequence and cidentifying an activity in a biological assay and identifying the protein in the supernatant condition, and electing an activity or a biological condition, the protein in the supernatant consequence in a cell, isolating the supernatant, and detecting an activity or a biological condition, for preventing, treating, or amelicating a custom and publication, such as cancer, inflammation and other immune condition, for preventing, treating, or amelicating a medical condition, such as cancer, inflammation and other immune condition, and blood clotting disorders (many examples are corrected condition). The nucleic acids are also useful for circumosome identification). The nucleic acids are also useful for circumosome identification, the polypeptides and antibodies are useful for tissues immunological probes for differential identification of the tissues immunological probes for differential identification of the circumosome identification, seads. The polypeptides and antibodies are useful for increase or decrease storage capabilities, fat content or other continuous in maniformal conditional companies. The present is a secreted protein of the 2 61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120 TGAALSSOGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 240 301 WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE 360 NLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE 330 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120 LVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP 300 GEFTCHARHPIGSQHVSLSISVHYSPKLIGPSCSWEAEGLHCSCSSQASPAPSLRWWLGE 480 481 ELLEGNSSQDSPEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGSILQLPDK 540 KGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINV 415 9 TGAALSSQCTKPTTSHFSVLSFTPRPQDHNTDLTCHVDFSRKGVSVQRTVRLVRVAYAPRD 1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW 161 NLGNGTSLPVLEGGSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVOVEHE 1 MLLPLILSSLIGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRODWTGSTPAYGYW 2; Indels 185; Gaps 6; Length 697; GEFTCHARHPLGSQHVSLSLSVHY------95.2%; Score 2576.5; DB 6; 73.0%; Pred. No. 7.4e-195; ive 1; Mismatches 2; LVISISRDNTPD------Best Local Similarity 73.0 Matches 509, Conservative Sequence 697 AA; 331 61 181 181 241 355 356 121 253 Query Match d à g 유 d ò g ð CC ઠે g à 엄 ò g 8 à δ

immune reactions to transplanted organs and tissues; such as host-versusCC graft and graft-versus-host diseases; or autoimmunity disorders;
cutoimmune infertility, Addison's Disease; haemolytic anaemia;
cantiphospholipid syndrome; rheumatoid arthritis; dermatitis; allergic
encephalomyelitis; glomerulonephritis; deodpasture's Syndrome; Graves'
CC encephalomyelitis; glomerulonephritis; Goodpasture's Syndrome; Graves'
CC bisease, Multiple Sclerosis; Mysthenia gravis; Neuritis; Ophthalmia;
CC bisease, Stiff-Man Syndrome; Polyendocrinopathies; Purpura; Reiter's
CC bisease; Stiff-Man Syndrome; autoimmune thyroiditis; Systemic Lupus
CC rinsulin dependent diabetes mellitus; autoimmune inflammatory eye
insulin dependent diabetes mellitus; autoimmune inflammatory eye
disease; lens tissue injury; demyellnation; systemic lupus erythematosus;
drug induced haemolytic anaemia; rheumatoid systemic lupus erythematosus;
and scleroderma. The present sequence is given in comparison with BGS-19
in the present invention.

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541 KGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINV 600
                                                                  VPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPBPKSSTQAPESQE
                                                                                                                601 VPTAGPLAQKRNQKATPNSPRTPLPPGAPSPBSKKNQKKQYQLPSPPBPKSSTQAPESQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human, cell surface protein, immunoglobulin, BGS-19, cytostatic, gynaecological, immunosuppressive, antiinflammatory, antiasthmatic, antidiabetic, dermatological; gene therapy.
                                                                                                                                                                                                 SQEELHYATLNFPGVRPRPBARMPKGTQADYAEVKFQ 512
                                                                                                                                                                                                                                    661 SQEELHYATLNFPGVRPRPBARMPKGTQADYAEVKFQ 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Siglec-10 amino acid sequence SEQ ID NO:7
                                                                                                                                                                                                                                                                                                                                                                                                                          ADD26582 standard; protein; 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-MAR-2003; 2003WO-US009676.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-MAR-2002; 2002US-0368422P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JAN-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GEFTCHARHPLGSQHVSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPAPSLRWWLGE 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---K 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MILPILLESELEGGGGAMDGRFWIRVQESVWVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ERGSYVRYNFMNDGFFLKVTALIQKPDVYIPETLEPGQPVTVICVFNWAFEECPPFSFSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271 NLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYPPRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 TGAALSSQGTKPTTSHFSVLSFTPRPQDHNTDLTCHVDFSRKGVSVQRTVRLRVAYAPRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 LVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----PPENLRVMVSQANRTVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLKVMVSQANRTVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481 ELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGSILQLPDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.2%; Score 2576.5; DB 7; Length 697; 73.0%; Pred. No. 7.4e-195; ive 1; Mismatches 2; Indels 185; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ 512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 73.0
Matches 509; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 697 AA;
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes human cell surface protein with gramehological, immunosuperssive, antianthamatory, antiasthmatic, antiaidabetic and dermatological activities, and can be used in gene therapy. (1) can be used for preventing, treating or ameliorating a medical condition, such as a disorder related to aberrant immunoglobulin cell surface.receptor activity; a cellular adhesion disorder; a disorder related to hyper- or hypo-immunoglobulin receptor activity; a cellular adhesion disorder; a disorder related to hyper- or hypo-immunoglobulin receptor activity; a disorder related to aberrant signal transduction; a reproductive disorder; cell surface.receptor activity; a cellular adhesion disorder; a disorder related to aberrant signal transduction; a reproductive disorder; cellular exproductive disorder; a permortional uterine bleeding; amenorthees; primary dysmenorthoes; exual dysfunction; infertility; pelvic inflammatory disease; placental aromactase deficiency; premature menopause; placental dysfunction; hormone deficiency; oestrogen deficiency; aberrant showing of female primary exual characteristics; aberrant showing of female primary exual characteristics; precocious puberty; precocious pecudopuberty; incomplete isosexual precocity; premature thelarche; premature adrenanche; premature pubarche; premature adrenanche; premature pubarche; premature adrenanche; premature pubarche; premature adrenanche; premature adrenanche; premature pubarche; premature adrenanche; premature adrenanche; premature adrenanche; premature adrenanche; premature adrenanche; premature pubarche; pelversity incomplete isosexual precocity; premature thelarche; dysmenorrhoea; hypomenorrhoea; pubarche; premature adrenanche; premature adrenanche; premature adrenanche; premature pubarche; premature adrenanche; archititis; asthma; immunodeficiency disease; such as AlDS; leukaemia; rheunatorid arthitis; agrandiomature disease; inflammatory bowel disease; sepsis; acne; neutrophilia; neutrophilia; neutrophilia; neutrophilia; neutrophilia
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New isolated nucleic acid molecule encoding BGS-19 polypeptides, useful for preventing, treating or ameliorating a medical condition, such as a disorder related to aberrant immunoglobulin cell surface receptor

Example 1; SEQ ID NO 7; 224pp; English.

activity

Chen J;

Wu S,

Siemers NO,

WPI; 2003-804052/75 Lee LM, Feder JN,

(BRIM) BRISTOL-MYERS SQUIBB

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SOBELHYATLINFPGVRPRPBARMPKGTQADYAEVKFQ 697

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241 İVİSİSRDNTPALEPQPQGNVPYLEAQKGQFLRILCAADSQPPATLSWVLQNRVLSSSHP 300
                                                                                                                                                                                                                                                  301 WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New PRO polypeptide, useful for diagnosing and treating a B cell related disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune mediated hemolytic anemia, myasthenia gravis or ankylosing spondylltis.
                             TGAALSSQGTKPTTSHFSVLSFTPRPQDHNTDLTCHVDFSRKGVSVQRTVRLRVAYAPRD
                                                                                                                                                                                                                                                                                                                                     TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
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                                                                                                                                                                                                                                                                                                                                                                                                           GEFTCHARHPLGSQHVSLSLSVHY---------
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ADL82805
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                                                                                                                                           원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to novel nucleic acids encoding human PRO secreted and transmembrane proteins. Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells for example proliferation, migration or differentiation) is typically governed by information is cecived from other cells and the immediate environment. The information is often transmitted by secreted purpoperides (for example information is often transmitted by secreted by properties (for example information is often transmitted by secreted by properties (for example intogenic factors, survival factors, cytotoxic factors, differentiation factors received from encourage and hormones) which are received and interpreted by diverse cell receptors or membrane bound proteins. These membrane bound proteins such as in the blocking of receptor-ligand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins, along with the CDNA sequences encoding them. The novel proteins of the invention may have cytostatic activities through the crimulation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or treating a tumour in a mammal. In addition, they may be useful for measuring or electing the expression of a tumour associated gene. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schoenfeld J, Wood W,
                                                                                                                                                                                               human, PRO; membrane bound protein; membrane bound receptor; cell proliferation; cell migration; cell differentiation; mitogenic factor; survival factor; cytotoxaic factor differentiation factor; neuropeptide; hormone; cell receptor; receptor-ligand interaction; cytostatic; chondrocyte; tumour.
                                                                                                                                                      Novel human secreted and transmembrane protein PRO 71236.
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  ADI37010 standard; protein; 697
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Matches 509;
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Claim 10; Fig 7; 695pp; English.

The present invention relates to PRO proteins and their coding sequences.

The PRO proteins are useful for diagnosing and treating a B cell related disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide antigen unresponsiveness, selective IgA deficiency, selective IgA deficiency, selective IgA deficiency, selective IgA deficiency with hypogammaglobulinemia of infancy, Burkitt's lymphoma, intermediate lymphoma, follicular lymphoma, type II lymphoma, intermediate lymphoma (Collicular lymphoma, type II lymphoma, intermediate lymphoma, pollicular lymphoma, type II hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic anxylosing spondylitis. The PRO proteins are also useful for preparing a condition that is responsive to the PRO protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO coding sequences are useful as hybridization probes in chromosome and gene mapping, in preparing PRO proteins, or in generating transgenic animals or knockout animals, which in turn are useful in the development and screening of therapeutically useful reagents.

Sequence 697 AA;

'n 240 252 270 330 354 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120 61 FKAVTETTKGAPVATNHQSREVEMSTRGREQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120 ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPBTLEPGQPVTVICVFNWAFEECPPPSFSW 180 121 ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW 180 301 WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE 360 361 NIGNGTSLPVLEGOSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHR 420 421 GEFTCHARHPLGSQHVSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPAPSLRWWLGE 480 356 KGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINV 415 601 VPTAGPLAOKRNOKATPNSPRTPLPPGAPSPESKKNOKKOYOLPSFPEPKSSTOAPESOE 660 9 9 1 MLLPLLSSLLGGSQAMDGRFWIRVQBSVMVPBGLCISVPCSFSYPRQDWTGSTPAYGYW 241 LVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP 1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW 181 TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 253 -----PPENERVMVSQANRTVLE 271 NLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE 481 ELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGSILQLPDK 541 KGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRIQTETPRPRFSRHSTILDYINV 416 VPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPESQE Gaps 2; Indels 185; 95.2%; Score 2576.5; DB 8; Length 697; 73.0%; Pred. No. 7.4e-195; ive 1; Mismatches 2; Indels 185; 476 SQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ 512 331 GEFICHARHPLGSQHVSLSLSVHY--------241 LVISISRDNTPD-------Best Local Similarity 73.0 61 121 355 Query Match

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respiratory-Gen; immundsuppressive; cerebroprotective; vasotropic; nootropic; antiallergic; cancer; bacterial infection; viral infection; neural disorder; immune system disorder; blood disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; inflammatory disorder; proliferative disorder; human. human secreted protein; cytostatic; antibacterial; virucide; neuroprotective; gynaecological; gastrointestinal-Gen; cardiant; cardiovascular-Gen; nephrotropic; antiinflammatory; muscular-Gen; Human secreted protein from gene 18 #3 ADD19314 standard; protein; 710 AA. 07-NOV-2001; 2001US-0331046P. (HUMA-) HUMAN GENOME SCI INC. 06-NOV-2002; 2002WO-US035606 (first entry) Rosen CA, Ruben SM; WPI; 2003-533050/50. N-PSDB; ADD19239 WO2003052377-A2. Homo sapiens 15-JAN-2004 26-JUN-2003. ADD19314; RESULT 7 ADD19314

The invention relates to an isolated nucleic acid molecule (cDNA)

Concing a human secreted protein, representing one of 8s novel genes.

Also included are recombinant vectors, host ceals (expressing the protein), the secreted proteins including their fragments, epitopes and homologues), an isolated antibody that binds specifically to the protein, diagnosing a pathological condition or susceptibility to a pathological condition based on the presence or absence of a mutation in the nucleic acid and diagnosing a condition based on the presence or absence of the mutation, diagnosing a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition a packed on the presence of a mount of expression of the protein in a biological sample and diagnosing a condition based on the presence or amount of expression of the protein in a biological sample of the protein, preventing, treating or amelicating a medical condition by administering the nucleic acid or protein to a mammalian subject, identifying a binding partner to the protein, the gene corresponding to the cDNA sequence, and identifying an activity in a biological assay of comprising expressing the nucleic acid in a cell, isolating the contractive detecting an activity in a biological assay and protein in the supernatant having the activity; . The nucleic acids the protein in the supernatant having the activity; of a cardiant, Cardiovascular cen, Nephrotropic, Antinflammatory, Muscular Gen, Respiratory-Gen, Immunosuppressive, Cerebroprotective, Vasotropic, Nortropic, Antiallergic. The methods and compositions of the present invention are useful for diagnosing, treating, preventing preventing preventing preventing preventing of sorders related to the novel polypeptides, such as cancer, bacterial or viral infections, and neural, immune system, blood, New isolated nucleic acids encoding signal transduction pathway component polypeptides, useful for diagnosing, treating, and/or preventing disorders, such as cancer, infections, cardiovascular and inflammatory Claim 11; SEQ ID NO 141; 554pp; English. diseases.

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                                                                                                                                                                                         29 GYGWEILDTSAGVSDGAGGLCISVPCSFSYPRODWTGSTPAYGYWFKAVTETTKGAPVAT
                                                                                                                                                                                                                      NHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYVRYNFMNDGF
                                                                                                                                                                                                                                                                              136 FLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSWTGAALSSQGTKPTTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           449 VSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPAPSLRWWLGEELLEGNSSQDSFEVT
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                                                                                                                                                             19 GRFWIRVQESVMVPE---GLCISVPCSFSYPRODWTGSTPAYGYWFKAVTETTKGAPVAT
                                                                                                                                                                                                                                        99 NHQSREVEMSTRGRPQLIGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYVRYNFMNDGF
                                                                                                                                                                                                                                                                                                          149 FLKVTALTOKPDVYIPETLEPGOPVTVICVFNWAFEECPPPSFSWTGAALSSQGTKPTTS
                                                                                                                                    Gaps
 muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, inflammatory or proliferative disorders (many examples of the diseases and disorders are given in the specification). The present sequence represents a novel secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sialic acid-binding Ig-related lectin; SIGLEC; asthma; system disease; leukaemia; allergy; inflammatory disease; damage; allergic rhinitis; osteoarthritis; Crohn's disease;
                                                                                                                                 10; Indels 188;
                                                                                                      Length 710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acid-binding Ig-related lectin, Siglec-BMS-L3a.
                                                                                                   Score 2417; DB 7;
Pred. No. 3.2e-182;
                                                                                                                                 3; Mismatches
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                                                                                                     89.3%;
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                                                                                                                                  481; Conservative
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                                                                                                                   Similarity
                                                                         Sequence 710 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUN-2002
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tissue
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The invention relates to an isolated SIGLEC (sialic acid-binding Igrelated lectin) protein (I). Pharmaceutical compositions comprising (I) are useful for treating immune system diseases such as asthma, leuksemia or other allergic or inflammatory diseases. Extracellular domains of (I) represent potential markers for screening, disagnosis, prognosis, follow-up assays, and imaging methods. (I) is useful as a target for drugs which inhibit inflammation, tissue damage and remodeling in asthma, and for inhibit inflammation, tissue damage and remodeling in asthma, and for inflammatory diseases such as allergic rhinitis, osteoarthritis, crohn's disease, psoriasis, rheumatorid arthritis, conjunctivitis, etc. (I) is also useful for monitoring the course of disease or disorders, and for identifying agents that bind with and/or modulate the biological activity of SIGLEC-BMS proteins. The nucleic acid molecules (II) encoding (I) are useful in diagnosis and/or prognosis methods, and to detect the presence and/or amount of SIGLEC-BMS nucleocide sequences and/or SIGLEC-BMS proteins in a biological sample. (II) are useful as nucleic acid probes are useful for screening genomic library to isolate a genomic clone of SIGLEC gene SIGLEC-BMS antibodies are also used to detect, sort or isolate cells expressing SIGLEC-BMS proteins and in diagnostic imaging technology.

AAUSTORY-AAUSTOSS represent human SIGLEC amino acid sequences of the
                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein molecules useful for treating immune system diseases such as asthma, leukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MILPILLSSILGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FKAVTETTKGAPVATNHOSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----VLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAFRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tch
al Similarity 75.1%; Pred. No. 2.2e-171;
452; Conservative 1; Mismatches 1;
psoriasis; rheumatoid arthritis; conjunctivitis.
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                                                                                                                                                                                                                                            (BRIM ) BRISTOL-MYERS SQUIBB CO.
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                                                                                                                                                                20-JUL-2001; 2001WO-US023082.
                                                                                                                                                                                                       21-JUL-2000; 2000US-0220139P.
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                                                                            WO200208257-A2
                                                                                                                                                                                                                                                                                        Longphre M,
                                                                                                                        31-JAN-2002
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New secreted and transmembrane polypeptides and their polynucleotides, useful for treating blood coagulation disorders, cancers and cellular
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N-PSDB; AAZ34109.
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                                                                                                                                                        243 WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 483 NOKKOYOLPSFPEPKSSTQAPESOESQEELHYATINFPGVRPRPEARMPKGTQADYAEVK 542
                                                                                                                                                                                                                                                                                331 GBFTCHARHPLGSQHVSLSLSVHYXKGLISTAFSNGAFLGIGITALLFLCIALIIMKILP
363 GBFTCHARHPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruman, PRO, EST; expressed sequence tag; PCR primer; hybridisation;
probe; blood coagulation disorder; cancer; cellular adhesion disorder;
secreted protein; transmembrane protein.
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                                                                                                                                                                                                                                                                                                                                                                                 423 KRRIQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKK
                                                                                                                                                                                                                                                                                                                                                                                                                                        451 NQKKQYQLPSFPEPKSSTQAPESQESQEBLHYATLNFFGVRPRPEARMPKGTQADYAEVK
                                                                                                                                                                                                         271 NLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE
                                                                                                                                                                                                                             303 NLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHB
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Chen J;

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The present invention describes secreted and transmembrane polypeptides and their polymouleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AAZ33891 to AAZ34338, and AA¥41685 to AA¥41774 represent polymucleotide and polypeptide sequence given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                    61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120
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74.8%; Pred. No. 2.4e-170;
ive 1; Mismatches 3;
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                               Claim 12; Fig 93; 530pp; English
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Matches 450; Conservative
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AAC78458 to AAC78599 represent polynucleotide and BST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bioactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bioactive molecules to cells. AAC78800 to AAC78897 represent PCR primers and probes used in the isolation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel PRO polypeptides and polynucleotides used in detection methods, 'target bioactive molecules to specific cells, and to modulate cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KP, Botstein D, Desnoyers L, Eaton DL;
E, Fong S, Gao W, Gerber H, Gerritsen ME;
FJ, Grimaldi CJ, Gurney AL, Hillan KJ;
Napler MA, Pan J, Paoni NF, Roy MA, Shelton Williams PM, Wood WI;
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                                         cytostatic;
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                                    otein; transmembrane protein; PRO; EST; tag; detection; cancer.
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             Human PRO940 (UNQ477) protein sequence SEQ
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                                                                                                                                                                                                 99WO-US005028.
99US-0123957P.
99US-01302432P.
99US-0131445P.
99US-0131445P.
99US-014569BP.
99US-014569BP.
99WO-US028313.
99WO-US028313.
99WO-US031243.
                                                                                                                                                                         2000WO-US004341
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Ferrara N, Filvaroff E, F
Goddard A, Godowski PJ, G
Kljavin IJ, Kuo SS, Napie
Stewart TA, Tumas D, Will
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N-PSDB; AAC78510.
                                           Human; secreted pro
expressed sequence
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28-APR-1999;
23-UUN-1999;
23-UUL-1999;
20-UUL-1999;
02-DEC-1999;
02-DEC-1999;
02-DEC-1999;
30-DEC-1999;
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Goddard A, G
Kljavin IJ,
Stewart TA,
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29-MAR-1999
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AAU29082 standard; protein; 544 AA. AAU29082;

(first entry) 18-DEC-2001

Human PRO polypeptide sequence #59.

PRO polypeptide; mammal; tumour; cancer; human; cattlo; horse; sheep; dog; cat; pig; goat; rabbit; tumour necroosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.

Homo sapiens.

WO200168848-A2.

20-SEP-2001

28-FEB-2001; 2001WO-US006520

2000WO-US005601 2000WO-US005841 2000US-0186968P. 000US-0189320P 000US-0189328P. 21-MAR-2000, 2000US-0190828P. 21-MAR-2000, 2000US-0191007P. 21-MAR-2000, 2000US-0191048P. 2000US-0187202P 01-MAR-2000; 02-MAR-2000; 14-MAR-2000; 15-MAR-2000; 06-MAR-2000; MESULT 11

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Sequence 544 AA;

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FKAVTETTKGADVATNHOSRBVERSTRGRFÖLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120

61

1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW 60

1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRODWIGSTPAYGYW

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The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when proliferation or differentiation of conditional part of stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adernal, hung, colon, cereat, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumors, such as prostate and breast tumors, in mammals and screen for modulators of the compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gurney AL;
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   Human; secreted and transmembrane protein: PRO; gene therapy; tumour necrosis factor-alpha release; TNF-alpha release; chondrocyte proliferation; chondrocyte differentiation; tumour; adreant tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; liver tumour.
                                                                                                                Novel human secreted and transmembrane protein PRO940.
                    ABU88006 standard; protein; 544 AA
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18-SEP-1997
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                                                                                                                                                           GEFTCHARHPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP 422
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                                                                                   NOKKOYOLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPRPBARMPKGTQADYAEVK
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                                                                       KRRIQIETPRPRESRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPPPPGAPSPESKK
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      Human secreted/transmembrane protein (PRO) #59.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ERGSYVRYNFWNDGFFLKYTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 TGAALSSOGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 240
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Pred. No. 2.4e-170;
1; Mismatches 3; Indels 140
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al Similarity 74.8%;
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Human; PRO; secreted protein; transmembrane protein; TNP-alpha; extracellular domain; tumour necrosis factor-alpha; TNP-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix; liver; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnerary; gene therapy.
   Human secreted polypeptide PRO940, SEQ ID NO:118.
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larity 74.8%; Pred. No. 2.4e-170;
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Best Local Similarity 73.2%;
Matches 510; Conservative 1
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Sequence 149, Appl
Sequence 7, Appli
Sequence 10, Appli
Sequence 259, App
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                                                                                           ; Search time 88.0765 Seconds (without alignments) 2053.348 Million cell updates/sec
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1 MLPLLLSSLLGGSQAMDGR......RPEARMPKGTQADYAEVKFQ 512
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/DSC_NEW_PUBCPP:*

3: /cgn2_6/ptodata/2/pubpaa/USO_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO_NEW_PUB.pep:*

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9: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*

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11: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*

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           GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-910-600-8
US-09-978-259-259
US-09-978-259-259
US-09-978-192A-259
US-09-978-1182A-259
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Maximum Match 100%
Listing first 45 summaries
                                                                  - protein search, using sw model
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1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
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Pred. No. 1e-177;
1; Mismatches 1; Indels 185;
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US-09-910-600-28
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121 ERGSYVRYNEMNDGFELKVTALTGKPDVYIPETLEPGGPVTVICVFNWAFEECPPPSFSW 180
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                                                                  181 TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPPRD
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Pred. No. 2e-177;
1; Mismatches 2; Indels 185;
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TITLE OF INVENTION: 12 Human Secreted Proteins
FILE REFERENCE: PF488P2
CURRENT APPLICATION NUMBER: US/09/984,130
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 60/243,792
PRIOR APPLICATION NUMBER: 60/243,792
PRIOR PILING DATE: 2000-10-30
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/108,407
PRIOR PILING DATE: 1999-10-27
PRIOR APPLICATION NUMBER: 60/105,971
PRIOR PILING DATE: 1999-10-27
PRIOR FILING DATE: 1998-10-28
PRIOR FILING DATE: 1998-10-28
NUMBER OF SEQ ID NOS: 149
(**) SOFTWARE: PatentIN Ver: 2.0
** SEQ ID NO 149
                                                                                                                                                                                                                                                                                                                                        331 GEFTCHARHPLGSQHVSLSLSVHY-----
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Publication No. US20030055231A1
GENERAL INFORMATION:
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Best Local Similarity 73.0%;
Fmatches 509; Conservative
                                                                                                                                    241 LVISISRDNTPD---
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Sequence 7, Application US/1040338
Publication No. US20040025195A1
GENERAL INFORMATION.
Publication No. US20040025195A1
GENERAL INFORMATION.
APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: NOVEL HUMAN CELL SURFACE PROTEIN WITH IMMUNOGLOBULIN FOLDS,
TITLE OF INVENTION: BGS-19
FILE REPERENCE: D0227 NP
CURRENT PRILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: U.S. 60/368,422
PRIOR APPLICATION NUMBER: U.S. 60/368,422
NUMBER OF SEQ ID NOS: 88
SOFTWARE: Patentin version 3.2
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1 MILPILLESELEGGSQAMDGRFWIRVQESVMVPBGLCISVPCSFSYPRODWTGSTPAYGYW
1 MILPILLESELEGGSQAMDGRFWIRVQESVMVPBGLCISVPCSFSYPRQDWTGSTPAYGYW
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US-10-403-938-7
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                                                                              Score 2576.5; DB 16; Length 697;
Pred. No. 2e-177;
1; Mismatches 2; Indels 185;
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APPLICANT: Chang, Han
APPLICANT: Chang, Han
APPLICANT: Mitney, Gena
TITLE OF INVENTION: NOVEL SIGLECS AND USES THEREOF
FILE REPRENCE: DO003NP
CURRENT APPLICATION NUMBER: US/09/910,600
CURRENT PILING DATE: 2001-07-20
PRIOR APPLICATION WUMBER: 60/220,139
PRIOR PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 32
SOOTWARE: Patentin Ver. 2.0
SEQ ID NO 8
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                                                                                 Query Match
Best Local Similarity 73.0%;
Matches 509; Conservative
ORGANISM: Homo sapien
      , ORGANISM: HOT
US-10-614-853-10
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FULLIAND NO. US20040138114A1
GENERAL INFORMATION:
PUBLICANT: HENRY CHUU
GENERAL INFORMATION:
APPLICANT: HENRY CHUU
APPLICANT: SHERMAN FONG
APPLICANT: SHERMAN FONG
APPLICANT: THOMS WODD
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61 FKAVTETTKGAPVATNHOSREVEMSTRGRFOLTGDPAKGNCSLVIRDAOMODESOYFFRV 120
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                                                                                                                                                                                                                                                              1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
                                                                                                                                                                                                      148;
                                                                                                                                        / Match 84.2%; Score 2278; DB 10; Length 544; Local Similarity 75.1%; Pred. No. 5.3e-156; les 452; Conservative 1; Mismatches 1; Indels 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 259, Application US/09978295A Patent No. US20020156006A1 GENERAL INFORMATION:
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Grimaldi, J. Christopher
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ilvaroff, Ellen
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Botstein, David
Desnoyers, Luc
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Bao, Wei-Qiang
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                           TYPE: PRT ORGANISM: Homo sapiens S-09-910-600-8
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IIILE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
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APPLICATION NUMBER: 60/064249
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APPLICATION NUMBER: 60/065311
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APPLICATION NUMBER: 60/066364
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APPLICATION NUMBER: 60/079294
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APPLICATION NUMBER: 60/079923
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                                                                                                                      Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
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Wood, William I.
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APPLICATION NUMBER: 60/
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FILING DATE: 1998-03-20
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llan, Kenneth
                   Ivar J.
                                                                                     Nicholas
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                                                   Mary A
                                                                               Paoni, Nic.
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FILING DATE: 1998-04-22
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391 KRRIQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPPGAPSPESKK 450
                                                                                  451 NOKKQYQLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK 510
                                                                                                                         483 NOKKOYOLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYABVK 542
                                      423 KRRIQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPPPPGAPSPESKK 482
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CURRENT FILING DATE: 2001-10-16
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Gurney, Austin L.
Hillan, Kenneth J
                                                                                                                                                                                                                                                                                                                Sequence 259, Application US/09978697
Patent No. US20320169284A1
GENERAL INFORMATION:
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FILING DATE: 2001-07-30
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PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR FILING DATE: 1997-11-21
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Williams, P. Mickey
Wood, William I.
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tewart, Timothy A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nicholas F
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PRIOR FILING DATE: 1998-03-13
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Filvaroff, Ellen
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Botstein, David
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PRIOR FILING DATE: 1997-10-3
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Paoni, Nic...
Pov, Margaret A
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FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/078910
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APPLICATION NUMBER: 60/080328
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APPLICATION NUMBER: 60/079294
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APPLICATION NUMBER: 60/079689
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APPLICATION NUMBER: 60/
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61 FKAVTETTKGAPVATNHQSREVENSTRGRPQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120 ERGSYVRYNFWNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW 180

1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW 61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV

1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW

1; Mismatches

450; Conservative

Matches

-------VLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 182

181 TGAALSSOGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD

121 ERGSYVTYNFMNDGFFLKVT-----

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243 WGFRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE 302

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------PPENLRVMVSQANRTVLE

183 LVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP 242

241 LVISISRDNTPD-------

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271 NLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE 330

423 KRRIQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPPPPGAPSPESKK 482

KRRIQIEIPRPRESRHSTILDYINVVPTAGPLAQKRNQKATPNSPRIPLPPGAPSPESKK 450

391

В 8 Б δ В

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483 NQKKQYQLFSFPEFKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK 542

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NOKKOYOLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK 510

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Fong, Sherman Gao, Wei-Qiang Gerber, Hanspeter Gerritsen, Mary E. Goddard, Audrey Godowski, Paul J. Grimaldi, J. Christopher Gurney, Austin L. Hillan, Kenneth J. Kljavin, Ivar J. Kuo, Sophia S. Napier, Mary A. Pan, James; Paoni, Nicholas APPLICANT: APPLICANT: APPLICANT: APPLICANT APPLICANT

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Score 2265; DB 9; Length 544; Pred. No. 4.6e-155;

83.7%; 74.8%;

Query Match Best Local Similarity

RESULT 8
US-09-978-192A-259
Sequence 259, Application US/09978192A
Facent No. US20020177553A1
FACENT No. US20020177553A1
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Berneyers, Luc
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang

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FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/081070
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PLICATION NUMBER: 60/082568
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APPLICATION NUMBER: 60/083558
                                                                        CATION NUMBER: 60/081049
                                                                                         FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081071
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APPLICATION NUMBER: 60/082804
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APPLICATION NUMBER: 60/083322
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APPLICATION NUMBER: 60/083496
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APPLICATION NUMBER: 60/083499
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APPLICATION NUMBER: 60/083559
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APPLICATION NUMBER: 60/084640
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FILING DATE: 1998-04-15
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                                                                                                            TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Title OF INVENTION: Acids Encoding the Same Fills of INVENTION: Acids Encoding the Same CURRENT APPLICATION NUMBER: US/09/978,192A

CURRENT FILING DATE: 2001-10-15

PRIOR FPLIATION NUMBER: 09/98885

PRIOR FILING DATE: 2001-07-30

PRIOR PLIATION NUMBER: 60/062250
                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PILING DATE: 1997-11-13
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FILING DATE: 1997-11-21
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APPLICATION NUMBER: 60/077632
FILING DATE: 1998-03-11
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PRIOR FILING DATE: 1998-03-11
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FILING DATE: 1998-03-13
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LICATION NUMBER: 60/079294
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FILING DATE: 1998-04-01
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                                                                          Williams, P. Mickey Wood, William I.
                   Shelton, David L.
Stewart, Timothy A.
Roy, Margaret Ann
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                                                       umas, Daniel
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APPLICANT: State Ann
APPLICANT: Shelton, David L.
APPLICANT: State and Timochy A.
APPLICANT: State and Timochy A.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wolliams, P. Mickey
APPLICANT: Wolliams, P. Mickey
APPLICANT: Wolliam I.
TITLE OF INVENTION: Secreted and Transmembrane FILE REFERENCE: P2630PL0-24
CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 1997-110-24
PRIOR FILING DATE: 1997-110-30
PRIOR FILING DATE: 1997-110-30
PRIOR FILING DATE: 1997-110-30
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-110-30
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                                                                                                                                                                                                                                                                              Sequence 259, Application US/09999832A Publication No. US20020192706A1 GENERAL INFORMATION:
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Pan, James,
Pani, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
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Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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Goddard, Audrey
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Kuo, Sophia S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ERGSYVTYNFMNDGFFLKVT------
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83.7%; Score 2265; DB 9;
Best Local Similarity 74.8%; Pred. No. 4.6e-155;
Matches 450; Conservative 1; Mismatches 3;
   PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598
PRIOR APPLICATION NUMBER: 60/084600
PRIOR PLING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-07
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PRIOR APPLICATION NUMBER: 60/08539
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83.7%; Score 2265; DB 9;
Best Local Similarity 74.8%; Pred. No. 4.6e-155;
Matches 450; Conservative 1; Mismatches 3; R APPLICATION NUMBER: 60/084627
R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/084643
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R APPLICATION NUMBER: 60/085339
R FILING DATE: 1998-05-13
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FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083499 APPLICATION NUMBER: 60/083558 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083559 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/084366 FILING DATE: 1998-05-05 APPLICATION NUMBER: 60/084414 FILING DATE: 1998-05-06 APPLICATION NUMBER: 60/08441 APPLICATION NUMBER: 00004637 FILING DATE: 1998-05-06 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/084639 FILING DATE: 1998-05-07 FILING DATE: 1998-05-15 APPLICATION UNMBER: 60/085704 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/085697 APPLICATION NUMBER: 60/083500 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083742 FILING DATE: 1998-05-13 APPLICATION NUMBER: 60/085323 FILING DATE: 1998-05-13 APPLICATION NUMBER: 60/085582 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/085689 APPLICATION NUMBER: 60/083554 APPLICATION NUMBER: 60/084640 APPLICATION NUMBER: 60/084598 60/085700 FILING DATE: 1998-04-30 1998-04-29 1998-04-29 FILING DATE: 1998-04-29 FILING DATE: 1998-05-07 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/ FILING DATE: 1998-05-07 PRIOR APPLICATION NUMBER: 60 PRIOR FILING DATE: 1998-05-1 FILING DATE: 1998-0. APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: 1998-01 APPLICATION NUMBER: FILING DATE: FILING DATE: FILING DATE: PRIOR
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61 FKAVTETTKGAPVATNHQSREVEMSTRGRPQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120

Gaps

~zz		AFFLICATION NOMBER: 80/ FILING DATE: 1997-11-13 APPLICATION NUMBER: 60/ FILING DATE: 1997-11-21	PRIOR APPLICATION NUMBER: 60/07745; PRIOR FILING DATE: 1998-03-10; PRIOR APPLICATION NUMBER: 60/07763; PRIOR FILING DATE: 1998-03-11	и шаш	R APPLICATION NUMBER: 60/ R FILING DATE: 1998-03-12 R APPLICATION NUMBER: 60/ R FILING DATE: 1998-03-13	R APPLICATION NUMBER: 60/ R FILING DATE: 1998-03-20 R APPLICATION NUMBER: 60/ R FILING DATE: 1998-03-20	R AFFLICATION NUMBER: BU/ R FILING DATE: 1998-03-20 R APPLICATION NUMBER: 60/ R FILING DATE: 1998-03-20	; PRIOR APPLICATION NUMBER: 60/07929; PRIOR FILING DATE: 1998-03-25	A AFFLICATION NUMBER: 60/ R FILING DATE: 1998-03-26 R APPLICATION NUMBER: 60/	; PRIOR FILING DATE: 1998-03-27; ; PRIOR APPLICATION NUMBER: 60/07968: PRIOR FILING DATE: 1998-03-27	; PRIOR APPLICATION NUMBER: 60/07966: ; PRIOR FILING DATE: 1998-03-27 ; PRIOR APPLICATION NUMBER: 60/079728	N N N	; PRIOR APPLICATION NUMBER: 60/079920; PRIOR FILING DATE: 1998-03-30; PRIOR APPLICATION NUMBER: 60/07992	FILING DATE: 1998-03-30 APPLICATION NUMBER: 60/	PRIOR FILING DATE: 1998-03-31 PRIOR APPLICATION UNMBER: 60/080107	4 AC 12	444	; PRIOR APPLICATION NUMBER: 60/08032'; PRIOR FILING DATE: 1998-04-01	PRIOR APPLICATION NUMBER: 60/080328 PRIOR FILING DATE: 1998-04-01 PRIOR APPLICATION NUMBER: 60/08033:	E AC	PRIOR FILING DATE: 1998-04-01 PRIOR APPLICATION UNMER: 60/081070	APPLICATION NUMBER: FILING DATE: 1998-04	APPLICATION NUMB
	181 TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 240	241 LVISISRDNTPD 252 183 LVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP 242	253PPENLRVMVSQANRTVLE 270 243 WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE 302	271 NIGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDFGVLELPRVQVEHE 330 	331 GEFTCHARHPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP 390	391 KRRIQTETPRPRESRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKK 450 	451 NQKKQYQLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPRPEARMFKGTQADYAEVK 510	511 PQ 512	543 FQ 544	0 8-189-259	259, Application No. US200:	ZANT: Ashkenazi, Avi CANT: Baker Kevin P. CANT: Botstein, David	Desnoyers Eaton, Da Ferrara	Filvaroff Fong, She				Hillan, Kenr Kljavin, Ive		Paoni, Ni Roy, Marg	CANT: Shelton, David L. Thought, Tinothy A.	Williams, P. Mickey Wood, William I.	NVENTION: 8
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271 NIGNGTSLPVLEGOSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE 330
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                                                                                                                                                                                                                                                                                      483 NOKKOYOLDEFPEPKSSTQAPESQESQEBLHYATLNFPGVRPRPEARMPKGTQADYAEVK
                                   303 NLGNGTSLPVLEGOSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE
                                                                                    331 GEFTCHARHPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP
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APPLICANT: Pan, James;
APPLICANT: Pan, James;
APPLICANT: Pan, James;
APPLICANT: Ray, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypep
TITLE OF INVENTION: Acids Encoding the Same
FILE REPREMENCE: P2630PLCLS
CURRENT APPLICANTON: NUMBER: US/09/978,585A
CURRENT APPLICATION NUMBER: US/09/978,585A
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 624
Prior Application removed - See File Wrapper or Palm
SEQ ID NO 259
LENGTH: 544
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Pred. No. 4.6e-155;
1; Mismatches 3;
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Goddowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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ilarity 74.8%;
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Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
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Gerber, Hanspeter
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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CORGANISM: Homo sapiens
US-09-978-585A-259
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APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: PS630PLC22
CURRENT APPLICATION NUMBER: US/09/978,608A
CURRENT FILING DATE: 2001-10-16
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Prior Application removed - See File Wrapper or Palm SEQ ID NO 259
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
                                              Sequence 259, Application US/09978608A Publication No. US20030045462A1 GENERAL INFORMATION:
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Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
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Best Local Similarity 74.8%;
Matches 450; Conservative
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Kuo, Sophia S.
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Baton, Dan
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FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120
                                                                                                                                                                                                                                                                                                                                                            ---VLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363 GEFTCHARHPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           423 KRRIQIETPRPRFSRHSTILDYINVVPTAGPLAOKRNOKATPNSPRTPPPFGAPSPESKK
                                                                 61 FKAVIETIKGAPVAINHQSREVEMSIRGRFQLIGDPAKGNCSLVIRDAQMQDESQYPFRV
                                                                                                                                               ERGSYVRYNFWINDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW
                                                                                                                                                                                                                                                                                       181 TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 LVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- PPENLRVMVSQANRTVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271 NLGNGTSLPVLBGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       303 NLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 331 GEFTCHARHPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP
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                                                                                                                                                                                                                 121 ERGSYVTYNFMNDGFFLKVT------
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Publication No. US20030050239A1
GENERAL INFORMATION:
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Shelton, David L.
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Williams, P. Mickey
                                                                                                                                                                                                                                                                                                                                                                                                                                          241 LVISISRDNTPD-----
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Filvaroff, Ellen
Fong, Sherman
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Gerritsen, Mary E
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Paoni, Nicholas F
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Desnoyers, Luc
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US-09-978-191A-259
, Sequence 259, Api
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IIILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IIILE OF INVENTION: Acids Encoding the Same
                                                               FILE REPERENCE: P2630P1C4
CURRENT APPLICATION NUMBER: US/09/978,191A
                                                                                                                                                 PRIOR FILING DATE: 2001-07-30
REICR APPLICATION NUMBER: 60/062250
RRICR APPLICATION NUMBER: 60/064249
RRICR APPLICATION NUMBER: 60/064249
RRICR FILING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
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PRIOR APPLICATION NUMBER: 09/918585
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APPLICATION NUMBER: 60/077649
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APPLICATION NUMBER: 60/078886
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APPLICATION NUMBER: 60/079656
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APPLICATION NUMBER: 60/079689
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APPLICATION NUMBER: 60/079663
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FILING DATE: 1998-03-31
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APPLICATION NUMBER: 60/080105
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APPLICATION NUMBER: 60
Wood, William I.
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TLE OF INVENTION: Acids Encoding the Same
LE REFERENCE: P2630P1C17
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URRENT FILING DATE: 2002-03-19
RIOR APPLICATION NUMBER: 09/918585
wence 259, Application US/09978403A
Lication No. US20030050240A1
ERAL INFORMATION:
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Gurney, Austin L.
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IOR APPLICATION NUMBER: 60/062250
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FILING DATE: 1997-11-03
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APPLICATION NUMBER: 60/077450
FILING DATE: 1998-03-10
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APPLICATION NUMBER: 60/066364
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Wood, William I.
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helton, David L.
tewart, Timothy A
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ilvaroff, Ellen
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                                                                                         Botstein, David
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                                                     PLICANT: Ashkenazi, Avi
PLICANT: Baker Kevin P.
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LICATION NUMBER: 60/079728
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APPLICATION NUMBER: 60/081195
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                                                                                                                                                                                                                                                                                                 243 WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                GEFTCHARHPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP 390
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                                                      TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
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CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
       121 ERGSYVTYNFMNDGFFLKVT---
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Wood, William I.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Shelton, David L.
Stewart, Timothy A.
                                                                                                                                                      241 LVISISRDNTPD-----
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Gerritsen, Mary E.
Goddard, Audrey
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Paoni, Nicholas F.
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Kuo, Sophia S.
Napier, Mary A.
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
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PRIOR APPLICATION NUMBER: 60/083496
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Search completed: November 5, 2004, 14:13:46 Job time: 92.0765 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 5, 2004, 13:50:17; Search time 17.7654 Seconds (without alignments) 3460.797 Million cell updates/sec Run on:

US-09-937-636-4 3377 1 MLLPLLLSSLLGGSQAMDGR.....RPEARMPKGTQADYAEVKFQ 639 Title: Perfect score: Sequence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUMMAKIES	Description	myelin-associated	myelin-associated	associ	ssoci	d cell	Schwann cell myeli	B isoform	differentiation		B-cell adhesion pr				B-cell adhesion		neural cell	neural cell	neural cell a	neural	biliary	**	hemicen	telencephal	T.	nephrin - human	neural cell	fasciclin II, tran	sciclin I	
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19;

Gaps

Query Match
Best Local Similarity 23.9%; Pred. No. 2.4e-24;
Matches 169; Conservative 100; Mismatches 256; Indels 182;

transient axonal g	axonal glycoprotei	protein-tyrosine k	transmembrane carc	vascular cell adhe	connectin/titin -	biliary glycoprote	connectin 3B - chi	biliary glycoprote	carcinoembryonic a	elastic titin - hu	protein-tyrosine-p	pregnancy-specific	fasciclin II precu	neural cell adhesi	probable neural ce
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2 A493	2 A346	2 JC4	2 C3	2 J	7 2	2 G	2	2	2	2	-1	2	2	<u>ا</u>	0
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ALIGNMENTS

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21 FWIRVO	J. Cell Biol. 104, 957-965, 1987 A;Title: The amino acid sequences of the myelin-associated glycoproteins: homology to the A;Reference number: A27185; MUID:87166195; PMID:2435742
69 KGAPVATNHOSREVERSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYVRY 128	A;Accession: AZ7165 A;Molecule type: mRNA A;Esidues: 1-66 cSAL> A;Crose-references: GB:X05301; NID:G56611; PIDN:CAA28920.1; PID:G56612
129 NFM 131	R;Sutcliffe, J.G.; Milner, R.J.; Shinnick, T.M.; Bloom, F.B. Cell 33, 671-682, 1983
128 TFSEHSVLDIVNTPNIVVPPEVVACTEVSCMVPDNCPELRPBLSWLGHEGLGEPAVLG 187	A.Titie: Identifying the protein products of brain-specific genes with antibodies to a A.Reference number: A90836; MUID:83259254; PMID:6347394
132NDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVISI 187 188 RLREDEGTWVQVSLLHFVPTREANGHRLGCQASFPNTTLQFEGYASMDVXYPPVIVEM 245	A;MCCESSIU: APUSANA A;MCLECESTURE TYPE: MRNA A;Residues: 'KS', 311-626 <sut> A;Cross-references: GB:V01544; GB:J00756; NID:g56879; PIDN:CAA24786.1; PID:g818027</sut>
188 SRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHPWGPRP 247	A.Experimental source: clone p18236 A.Note: the authors translated the codon CAG for residue 350 as Asn R.Bloom, F.E.; Battenberg, B.L.F.; Milner, R.J.; Sutcliffe, J.G. J. Neurosci. 5, 1781-1802, 1985
248 LGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLENLGNG 307 	A,Title: Immunocytochemical mapping of 18236, a brain-specific neuronal polypeptide dega A,Reference number: IS6564, MUID:85263773; PMID:4020419 A,Accession: I56564 A,Status: preliminary; translated from GB/EMBL/DDBJ
308 TSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTC 367	A;Molecule type: mRNA A;Residues: 'KS',311-626 <res> A;Residues: 'KS',311-626 <res> A;Cross-references: GB:346702; NID:g203181; PIDN:AAA40831.1; PID:g203182 R;Sutciliffe, J.G.; Milner, R.J.; Bloom, F.E.</res></res>
368 HARHPLGSQHVSLSLSVHYSPKLLGPS-CSWEABOLHCSCSSQASPAPSLRWMLGBELLE 426 	Cold Spring Harb. Symp. Quant. Biol. 48, 477-484, 1983 Affitle: Cellular localization and function of the proteins encoded by brain-specificoma. A.Reference number: 152892; MUID:84206577; PMID:6586369 A.Accession: 152892
427 GNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCBAWNVHGAQSGSLLQLPDKKGLI 486	A.Status: preliminary; translated from GB/EMBL/DDBJ A.Molecule: YS: 311.626 < RE2> A.Cross-references: GB:M11721; NID:g206780; PIDN:AAA42082.1; PID:g206781
487 STAFSNGAPLGIGITALLELCLALIIMKILPKRRTQTBTPRPRPSRHSTILDYIN 541	C;Comment: The sequence contains five presumably extracellular domains that are dispared C;Comment: The long form predominates in early postnatal life; alternative splicingaprod C;Comment: The papers cited variously predict the mature protein to begin at residue five C;Genetics:
542 VVPTAGPLAQKRNQKATPNSPRTPLPPGAPSP-ESKGNQKQYQLPSFPE 590 550AGDNPPVLFSSDFRISGAPEKYESERRLGSERRLGL 586	A;Gene: MAG A;Amp position: 7 C;Superfamily: myelin-associated glycoprotein; immunoglobulin homology C;Keywords: alternative splicing; brain; cell adhesion; duplication; glycoprotein; teans
591 PKSSTQAPESQESQEELHYATLNFPGVRPRFEARMPKGTQADYAEVK 637 : : : : : 587RGEPPELDLSYSHSDL-GKRPTKDSYTLSEELAEYAEIR 624	Fil-19/Jomain: signal sequence #status predicted <51G> Fig-2626/Product: myelin-associated glycoprotein, long splice form #status predicted Fig-102/Jomain: immunoglobulin homology <1MM1> Fil8-120/Region: cell attachment (R-G-D) motif Fil5-219/Domain: immunoglobulin homology <1MM2>
	S254-30// DOMAIN: IMMUNOQLODUIN HOMOLOGY STRIMS

myelin-associated glycoprotein precursor, long splice form - rat
NyAlternate names: 18256, brain neuron cytoplasmic protein 3; MAG
NyAlternate names: 18256, brain neuron cytoplasmic protein 3; MAG
Chate: 19-Reb-1984 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
Chate: 19-Reb-1984 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
Chate: 19-Reb-1984 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
NyAltai, C.; Brow, M.A.; Nave, K.A.; Noronha, A.B.; Quarles, R.H.; Bloom, F.E.; Milner, R.Picc. Natl. Acad. Sci. U.S.A. 84, 4337-4341, 1987
A.Stiller Two forms of 18236/myelin-associated glycoprotein, a cell adhesion molecule for A.Reference number: A29028, MUID:87232001; PMID:2438699 A, Molecule type: mRNA
M. Residues: 1-626 < LALI.
M. Residues: 1-626 < LALI.
M. Residues: 1-626 < LALI.
M. Residues: 1-626 < LALI.
M. Roder, U. P. Chia, L. S.; Down, U.; Wilkinson, D.; Bayley, H.; Braun, P.; Du Foe, Natl. Acad. Sci. U. S. A. 84, 600-604, 1987
M. M. Molecular cloning and primary structure of myelin-associated glycoprotein.
M. Reference number: A94175; MUID: 87092455; PMID: 2432614 A.Residues: 1-626 <ARQ> A Molecule type: mRNA

"ArCross-references: GB:M14871; NID:g205267; PIDN:AAA41556.1; FID:g205268 R.R.Salzer, J.L.; Holmes, W.P.; Colman, D.R.

perfamily: myelin-associated glycoprotein, immunoglobulin homology synotds: alternative splitchis, teladosin; transine 19/Domain: signal sequence #status predicted <SIG>.
19/Domain: signal sequence #status predicted <SIG>.
626/Product: myelin-associated glycoprotein, long splice form #status predicted < tatus: preliminary; translated from GB/EMBL/DDBJ
colecule type: mRNA
esidues: YKS'. 311-626 xRES>
esidues: YKS'. 311-626 xRES>
toss-references: GB:M35702; NID:g203181; PIDN:AAA40831.1; PID:g203182
utcliffe, J.G.; Milner, R.J.; Bloom, F.E.
d Spring Harb. Symp. Quant. Biol. 48, 477-484, 1983
it.e: Callular localization and function of the proteins encoded by brain-specificing
eference number: I52892; MUID:84206577; PMID:6586369 operimental source: clone p18236

Ste: the authors translated the codon CAG for residue 350 as Asn

Loom, F.B.; Battenbergy E.L.F.; Milner, R.J.; Sutcliffe, J.G.

Neurosci. 5, 1781-1802, 1985

Tele: Immunocytcohemical mapping of 18236, a brain-specific neuronal polypeptide degon

sference number: 156564; MUID:85263773; PMID:4020419 coss-references: GB:M11721; NID:g206780; PIDN:AAA42082.1; PID:g206781
noment: The sequence contains five presumably extracellular domains that are discarding a nument: The long form predominates in early postnatal life; alternative splicinging noment: The papers cited variously predict the mature protein to begin at residue.10 F;425-490/Domain: immunoglobulin homology <IMM5>
F534-536/Domain: transmenbrane #status predicted <IMM>
F;537-626/Domain: intracellular #status predicted <INT>
F;597-223,246,315,332,406,450,454/Binding site: carbohydrate (Asn) (covalent) #statusippe . 33, 671-682, 1983 tle: Identifying the protein products of brain-specific genes with antibodies to construct and the materian and the material and the materi >lecule type: mRNA
ssidues: 'KS',311-626 <SUT>
coss-references: GB:V01544; GB:J00756; NID:g56879; PIDN:CAA24786.1; PID:g818027 131 128 TPSEHSVLDIINTPNIVVPPEVVAGTEVEVSCANVPDNCPELRPELSWLGHEGLGEPTVLG 187 132 ----NDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVISI 187 10 FWIMISASRGGHWGAWMPSSISAFEGTCVSIPCRFDFP--DELRPAVVHGVWYFNSPYPK 67 21 FWIRVQ------ESVMVPEGLCISVPCSFSYPRODWIGSTPAYGYWFKAVTETT 69 KGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYVRY coss-references: GB:X05301; NID:g56611; PIDN:CAA28920.1; PID:g56612 Atcliffe, J.G.; Milner, R.J.; Shinnick, T.M.; Bloom, F.E. 260; Indels 172; Length 626; 14.2%; Score 479; DB 1; ilarity 23.6%; Pred. No. 7.9e-24; Conservative 104; Mismatches 260; atus: preliminary; translated from GB/EMBL/DDBJ lecule type: mRNA sidues: 'KS',311-626 <RE2> immunoglobulin homology <IMM2> immunoglobulin homology <IMM3> immunoglobulin homology <IMM4> immunoglobulin homology <IMM4> .-102/Domain: immunoglobulin homology <IMM1> 8-120/Region: cell attachment (R-G-D) motif Similarity cession: A90836 129 NFM---2-219/Domain: -307/Domain: p position: 7 Best Local Simi Matches 166; Query Match netics: g 셤 ð à ò 셤

^M⁷

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myelin-associated glycoprotein - mouse myelin-associated glycoprotein - mouse)
(S.Species: Mus musculus (fhouse mouse)
(S.Species: Musculus (fhouse mouse)
(S.Species: 33-Mar-1990 #sequence revision 23-Mar-1990 #text_change 23-Jul-1999
(S.Accession: B33785; A33785; S05687; S02374
(S.Mayano, R., Sakimura, R.; Inuzuka, T.; Takahashi, N. Biochem. Biophys. Res. Commun. 165, 1162-1169, 1989
A,Title: cDNA cloning of mouse myelin-associated glycoprotein: a novel alternative splic: A,Reference number: A33785; MUD:90121220; PMID:2482022
A,Scatus: preliminary
                                                                                                                                                                                                     (covalent) #status pred
  short splice form #status predicted
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                                                                                                                                                                                                                                                                                          Indels 129;
F;20-582/Product: myelin-associated glycoprotein, short splice form $7.51-10.7 Domain: immunoglobulin homology <IMM1>
F;118-120/Region: cell attachment (R-G-D) motif F;118-120/Region: cell attachment (R-G-D) motif F;152-219/Domain: immunoglobulin homology <IMM2>
F;254-30/7Domain: immunoglobulin homology <IMM3>
F;340-394/Domain: immunoglobulin homology <IMM4>
F;425-490/Domain: immunoglobulin homology <IMM4>
F;541-580/Domain: transmembrane #startus predicted <ITMN>
F;537-582/Domain: intracellular #status predicted <ITMN>
F;99,223,246,315,332,406,456,450,454/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                               Length 582;
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                                                                                                                                                                                                                                             13.9%; Score 469.5; DB 1; 24.7%; Pred. No. 3e-23; ive 89; Mismatches 226;
                                                                                                                                                                                                                                               Query Match
Best Local Similarity 24.7<sup>1</sup>
Matches 146; Conservative
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A,Residues: 1-637 <FUJ>
A,Cross-references: GB:M31811
A,Accession: A33785
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NyAlternate names. 1B236; brain neuron cytoplasmic protein 3; MAG
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 16-Jun-2000
C;Accession: B29028; B27185; A60055
R;Lai, C.; Brow, M.A.; Nave, K.A.; Noronha, A.B.; Quarles, R.H.; Bloom, F.E.; Milner, R.
Proc. Natl. Acad. Sci. U.S.A. 84, 4337-4341, 1987
A;Title: Two forms of 1B236/myelin-associated glycoprotein, a cell adhesion molecule for A;Reference number: A29028; MUID:87232001; PMID:2438699
A;Accession: B29028
A;Molecule type: mRNA
A;Residues: 1-582 cLAI>
A;Cross-references: GB:MA2357; NID:g205271; PIDN:AAA41558.1; PID:g205272
R;Salzer, J.L.; Holmes, W.P.; Colman, D.R.
J. Cell Biol: 104, 957-965, 1987
A;Title: The amino acid sequences of the myelin-associated glycoproteins: homology to the A;Reference number: A27185; MUID:87166195; PMID:2435742
A;Reference number: A27185; MUID:87166195; PMID:2435742
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;1-19/Domain: signal sequence #status predicted <SIG>
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                                                                                                                                                                                                                               TSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTC 367
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    RIREDEGTWVQVSLLHFVPTREANGHRLGCQAAFPNTTLQFEGYASLDVKYPP--VIVEM 245
                                                 SRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHPWGPRP 247
                                                                                                                                       LGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLENLGNG 307
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the long form predominates
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A; Residues: 419-582 <8AL>
A; Residues: 419-582 <8AL>
A; Cross-references: GB:X06554; NID:956614; PIDN:CAA29797.1; PID:91334302
R; Tropak, M.B.; Johnson, P.W.; Dunn, R.J.; Roder, J.C.
R; Tropak, M.B.; Johnson, P.W.; Dunn, R.J.; Roder, J.C.
A; Title: Differential splicing of MAG transcripts during CNS and PNS deve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---FQGAHRLMWAKIGPVGAVVAFAILIAIVCYITQTRRKKNVTBSPSFS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---RGEPPELDLSYSHSDL-GKRPTKDSYTLTEELAEYAEIR 624
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A,Molecule type: mRNA
A,Rediecule type: RNA
C,Comment: The sequence contains five J
C,Comment: The short form is found in it
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301 PTTGSASPKHQKKSKLHGP-
1988
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Best Local Similarity 21.3%;
Matches 148; Conservative
                                                        A; Accession: A30521
                                                                                                                                                   A; Gene: GDB:CD33
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                                Across-references: GB:M31811; NID:g199016; PIDN:AAA39487.1; PID:g199017
R.B.Dilta, N.; Sato, S.; Kurihara, T.; Inuzuka, T.; Takahashi, Y.; Miyatake, T.
Essa. Lett. 232, 323-327, 1988
A. Title: Developmentally regulated alternative splicing of brain myelin-associated glyco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 RLREDEGTWVQVSLLHFVPTREANGHRLGCQAAFPNTTLQFEGYASLDVKYPP--VIVEM 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 ----NDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVISI 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 SRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHPWGPRP 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 LGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLENLGNG 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          308 ISLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTC 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 NSS-------VEALEGSHVSLLCGADSNPPPLLTWMRDGMVLREA---VAKS 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               427 GNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGSILQLPDKKGLI 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 NYPPVVFKSRTQVVHESFQGRSRLLGDLGLRNCTLLLSTLSPELGGKYYFRGDLGGYNQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     368 HARHPLGSOHVSLSLSVHYSPKLLGPS-CSWEAEGLHCSCSSOASPAPSLRWWLGEELLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 FWIRVQES-------VMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWFKAVTETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 FWIMISASRGGHWGAWMPSTISAFEGTCVSIPCRFDFP--DELRPAVVHGVWYFNSPYPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 KGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYVRY
                                                                                                                                                                                                                                                                                                                         ersuperfamily: myelin-associated glycoprotein; immunoglobulin homology chreywords: alternative splicing; glycoprotein; transmembrane protein fail52-219/Domain: immunoglobulin homology <IMM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         288 LYLDLEEVTPGEDGVYACLAENAYGQDNRTVELSVMYAPWKPTV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 129;
                                                                                                                                                                                                                                                                                                                                                                                                      Length 637;
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                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 13.8%; Score 466.5; DB 2; Best Local Similarity 24.6%; Pred. No. 5.4e-23; Matches 145; Conservative 91; Mismatches 225;
                                                                                                                                                 %,Molecule type: mRNA
,AyResidues: 310-374,566-573,584-588 <FU2>
,AyCross-references: EMBL:X07849
                                                                                                                                                                                                                          A Molecule type: mRNA
A,Residues: 310-374;566-582 <FU4>
A,Cross-references: EMBL:X07849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 NFM---
                                                                                                                                 A.Accession: S05687
                                                                                                                                                                                                              ApAccession: S02374
                                                                                                                                                                                                                                                                                                         Map position: 7
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A,Title: Isolation of a cDNA encoding CD33, a differentiation antigen of myeloid progenio
A,Reference number: A30521, MUID:89009814, PMID:3139766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |||| :|:: : ||
BRGS-TXYSYKSPQLSVHVTDLTHRPKILIPGTLEPGHSKNLTCSVSWACEQGTPPIFSW 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 LSAAPTSLGPRTTHSSVLIITPRPODHGTNLTCQVKFAGAGVTTERTIQLNVTYVP---- 235
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    VLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLV 184

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EFTCHARHPLGSQHVSLSSVHYSPKLLGPSCSWEAEGLHCSCSSQASPAPSLRWWLGEE 423
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                                                                                                                                                                                                                                                                                                           A,Cross-references: GDB:119762; OMIM:159590
A,Cross-references: GDB:119762; OMIM:159590
A,May position: 19q13.3-19q13.4
C;Keywords: glycoprotein; surface antigen; transmembrane protein
F;1-17/Domain: signal sequence #status predicted <SIG>
F;1-259/Domain: extracellular #status predicted <EXT>
F;260-282/Domain: transmembrane #status predicted <TWM>
F;283-364/Domain: intracellular #status predicted <TWM>
F;283-364/Domain: intracellular #status predicted <TWM>
F;100,113,160,209,230/Binding site: carbohydrate (Asn) (covalent) #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.4%; Score 451.5; DB 2;
21.3%; Pred. No. 2.6e-22;
live 49; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            604 QEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ 639
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                                                                                                                A;Molecule type: mRNA
A;Residues: 1-364 <SIM>
A;Cross-references: UNIPROT:P20138
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RESULT O

"Mobility cell surface antigen CD33 precursor - human "Mobility cell surface antigen CD33 precursor - human "Mobility cell surface antigen (man) (Mobility cell 2004 - Mobility cell 2004 - Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility cell 2007 | Mobility c

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the myeloid CD33 anti
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C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | :|||::
VREPFVRYSYKKSQLSLHVTSLSRTPDIIIPGTLEAGYPSNLTCSVPWACEQGTPPTFSW 179
                                                                                                574 GAMERWAL----GVKEGSGAP--QEVIPTSH------PPMKP----TKGPLEDPPBYAEIR 618
                                                                                                                                                                                                                                                                                                                   m33-B isoform - mouse
C;Species: Mus sp. (mouse)
C;Species: Mus sp. (mouse)
C;Accession: 152590
R;Tchilian, E.Z.; Beverley, P.C.; Young, B.D.; Watt, S.M.
Blood 83, 3188-3198, 1994
A;Title: Molecular cloning of two isoforms of the murine homolog of the myel
A;Reference number: 152590; MUID:94250900; PMID:8193354
A;Accession: 152590
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C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 149583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 MSTALISLSSRIIDSSVLIFIPQPQDHGIKLICLVIFSGAGVIVERTIQLNVIRKSGQMR
                                                    --KKQYQLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---VLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP---R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MIMPLPLPLICAGSLAQDLEFQLVAPESVTVEEGLCVHVPCSVFYPSIKLT-LGPVTGSW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GB:S71345; NID:g551352; PIDN:AAB30842.1; PID:g551353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.2%; Score 311; DB 2; Length 862;
21.5%; Pred. No. 1.2e-12;
tive 97; Mismatches 276; Indels 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72; Indels
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1. Inmunol. 151, 175-187, 1993

A) Title: Organization of the murine Cd22 locus. Mapping the Aprice of the murine Cd22 locus. Mapping the Aprice of the murine Cd22 locus. Mapping the Aprice of the murine Cd22 locus. Mapping the Aprice of the murine Cd22 locus. Mapping the Multiple of the Multiple of the Aprice of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Multiple of the Mul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-403 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERGSYVRYNFMNDGFFLKVT----
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Best Local Similarity 36.99
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240 ELVL 243
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Schwann cell myelin protein precursor - Japanese quail
C;Species: Coturnix coturnix japonica (Japanese quail)
C;Date: 17-U1-1992 #Sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: JH6093; PS0356
R;Dulac, C.; Tropak, M.B.; Cameron-Curry, P.; Rossier, J.; Marshak, D.R.; Roder, J.; Le
Neuron 8, 32-334, 1992
A;Title: Molecular characterization of the schwann cell myelin protein, SMP: structural
A;Reference number: JH6093; MUID:92153423; PMID:1739462
A;Accession: JH6093
A;Molecule type: mRNA
A;Residues: 1-620 «DUJ.
A;Cross-references: UNIPROT:Q92154; GB:S83711; NID:g245729; PIDN:AAB21466.1; PID:g245736
A;Molecule type: mRNA
A;Residues: UNIPROT:Q92154; GB:S83711; NID:g245729; PIDN:AAB21466.1; PID:g245736
A;Rote: the species of quail is not identified
A;Rote: the species of quail is not identified
A;Rotes: 18-31;119-132;135-157;563-569, X*, S71 «DUL1»
C;Comment: This protein
A;Residues: 18-31;119-132;135-157;563-569, X*, S71 «DUL1»
C;Comment: This protein is expressed on all external membranes of Schwann cells.
C;Superfamiliy: myellin-associated glycoprotein; immunoglobulin homology cikeywords: glycoprotein; transmembrane #status predicted «SIG»
F;1-17/Domain: signal sequence #status predicted «SIG»
F;1-17/Domain: signal in munoglobulin homology ciMM»
F;202-314,331,405,449/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292 MVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGV 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               274 RGSEVLREE---PGRNLRLLLSNVGPDDGGSFSCVAENRHGRHNRSLQLRVAYAP---RA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               411 SPAPSLRWWLGEELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        436 IPDSSLVFELPTRNQTVSDGHRDFTAAPPGSDGSITGILTLRGPLEPRLLVLCAARNRHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     471 AQSGSILQLPDKKGLISTAFSNGAFLG-IGITALLFLCLALIIMKILPKRRTQTETPRPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 LVLTVLLMGTGCISAPWAAWMPPKWAALSGTCVQLPCRFDYPEE----LRPASIGGLWY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 AVTETTKGAP-----VATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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ilarity 23.5%; Pred. No. 4e-18;
Conservative 89; Mismatches 270; Indels 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 -SQYFFRVERGSYVRYNF
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Best Local Similarity
Matches 169; Conserv
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62 KAVTETTKGAPVATNHQSREVEMSTRGREQLTGDPAKGNCSLVIRDAQMQDESQYFFRVE 121 69 DKATKKFKGT-VLYNKABP	136 FLKVTVLSFTPRPQDHVTDLTCHVDFSRKGVSAQRTVRL 174	175 RVAYAPALEPQPQ 200 246 DVKYTPKLBIKVNPTEVEKNNSVIMTCRVNSSNPKLRTVAVSWFKDGRPLEDQELEQEEQEQQ 305	201AQKGQFLR 215 306 MSKLILHSVTKDWRGKYRCQASNDIGPGESEEVELTVHYAPEPSRVHIYPSPAEEGQSVE 365	216 LLCAADSQPPAT-LSWVLQNRVLSSSHPWGPRPLGLELPGVKAGDSGRYTCRAENRLG 272	273SQORALDLSVOYPPENLRVMVSQANRTVLENLGNGTSLPVLBGGSLCLVCVTHSSPPA 330 421 KIDQEAKLDVHYAPKAVTTVIQSFTPILEGDSVTLVCRYNSSNPD 465	331 RLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEPTCHARHPLGSQHVSLSLSVHY 386 	387 SPKLLGPS	402LHCSCSSQASPAPSLRWWLGEELLEGNSSQDSFEVTPSSA 441 	442 GPWANSS-LSIHGGLSSGLRLRCEAWNVHGAQSGSILQLPDKKGL 485	486 ISTAFSNGAFLGIGITALLFLC-LALLIMKILPKRRTQTETPRPRFSRHSTILDYIN 541 : : : : :	542 VVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEP 591	592KSSTQAPESQES	EARMPKGTQADYAEVK 637 : : : QAKEDVDYVTLK 861	
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Length 868; A;Molecule type: nucleic acid A;Residues: 1-868 470R> A;Experimental source: B cell lymphoma 38C13 A;Note: sequence extracted from NCBI backbone (NCBIP:116156) DB 2;

276 MTCRVNSSNPKLRTVAVSWFKDGRPLEDQELEQEQQMSKLILHSVTKDMRGKYRCQASND 335 295 QANRIVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARLS--WTQR--GQVLSPSQPSDPG 350 441 KAVITVIOSF-----TPILEGDSVTLVCRYNSSNPDVTSYRWNPQGSGSVLK-----PG 489 394 490 VLRIQKVTWD-SMPVSCAACNHKCSWALPVILNVHYAPRDVKVLKVSPASEIRAGQRVLL 548 549 OCDFAESNPAEVRFFWKKNGSLVQEGRYLSFGSVSPEDSGNYNCMVNNSIGETLSQAWNL 608 -----GEELLEGNSSQDSFEVTPSSAGP-----WANSS-LSLHGGLSSG 458 609 QVLYAPRRLRVSIIPGDHVMEGKKATLSCE---SDANPPISQYTWFDSSGQDLH---SSG 662 LRLRCEAMNV------HGAQSG-----SILQLPDKKGLISTAFSNGAFLGIGI 500 ---YVR 127 98 KOGRVTFLGNRI-DNCTLKIHPIRANDSGNLGLRMTAGTERWMEPIHLNVSEKPFQPYIQ 156 157 MPSEIRESQSVTLICGLNFSCFGYDILLKWFLEDSEITSITSSVTSITSSVTSSIKAVYT 216 141 --VLSFTPRPQDENTDLTCHVDFSRKGVSAQRTVRLRVAYAP--------- 180 ---GNVPYLE--------AQKGQFLRLLCAADSQPPAT-LSWVLQNRVLS 238 336 IGPGESEEVELTVHYAPEPSRVHIYPSPÄEEGÖSVELICESLASPSÄTNYTÄYHNRKPIP 395 239 SSHPWGPRPLGLELPGVXAGDSGRYTCRAENRLG----SQQRALDLSVQYPPENLRVMVS 294 -----LHCSCSSQASPAPSLRWWL 420 TALLFLCLALIIMKILPK---RRTQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKA 557 716 CLTIFI-LAIWGMKIQKKWKQNRSQQGLQE-------NSSGQSFFVRNKKA 758 558 TPNSPRTPLPPGAPSPESK-----KNOKKOYQLPSFPEPKS-----STQAPESOE 602 ----QEELHYATLNFPGVRPRPEARMPKGTQADYAEVK 637 759 R----RIPLSEG---PQSQGCYNPAMDDIVSYAILRFPESDIHNAGDAGIPATQAPPNN 811 38 EGACIRIPCKYKTPLPKARLDNILLPONYEFDKATKKFTGTCLYNATKTEKDPESELYLS 97 33 EGLCISVPCSFS--YPRODWIGSTPAYGYWFXAVTETTKG----APVAINHQSREVEMS VLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYSP---KLLGPS------Indels 365; ----YN-----FMNDGFFLKVT----TRGREQLIGDPAKGNCSLVIRDAOMODESQYFFRVERGS----9.0%; Score 305.5; DB 2; llarity 21.3%; Pred. No. 2.9e-12; Conservative 92; Mismatches 251; -RDLVISISRDNTP----ALEPQPQ e03 S-----Query Match Best Local Similarity Matches 192; Conserv 86 128 181 201 396 351 395 421 459 501 812 ठ ò 셤 ò 셤 à a ò g ò 원 ò g ò g ⋧ g ò g à CD Š Ω ð g q ò ð

RESULT 10 JH0371 B-cell adhesion protein CD22 beta splice form precursor - human

N;Alternate names: B-cell membrane protein CD22 C.Species: Homo sapiens (man) C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004	OY 327 SPPARLSWTORGOVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSV 384
:	385 HYSPKILGPSCSWEAEGLHCSCSSQASPAPSLRWWLGEELLEGNSSQDSFE-
A/intle: cUnA cloning of the B cell memorane protein CD22: a mediator of B-B cell intera A/Reference number: JH0371, MUID:91086838; PMID:1985119 A/Accession: JH0371	DD SOZ QYAPKDVKVKRIKFLSEIHSGNSVSLQCDFSS-SHFKEVQFFWENNGKLLGKESQLNFUS SOU OV 436 VTPSSAQPWANSSLSLHGGLSSGLHGGESSG
	::
A.Cross-references: UNIPROT:060926; GB:X59350; NID:936090; PIDN:CAA42006.1; PID:936091 A.Experimental source: B lymphocyte A.Necte: the authors translated the codon AAT for residue 358 as Met B.Milon C.T. Waifold W. Vollon F. Mannion T. Wand B. Whyl T. B. Willow C.T. Waifold W. Vollon F. Mannion T. Wand B. Whyl T. B.	Qy 466TA 489 Qy 166TA 489 An abstract material of the control of th
the human CD22 gene	490 FSNGAFLGIGITALLFLCLALLIMKILPKRRTQTETPRPRFS
A.Accession: 156171 A.Status: translated from GB/EMBL/DDBJ	678 YYSPETIGRRVAVGLGSCLAILILAICGLKLQRRWKRTQSQGLQENSSGQSFFVRNKKV
A;Molecule type: DNA A;Residues: 121-269,'T',271-473,'K',475-614,'R',616-638,'Y',640-711,777-847 <wil2> A;Cross_references: GB:S61375; NID:g385980; PIDN:AAC18956.1; PID:g3184492</wil2>	Qy 532 RHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESK 576 ::::::: :: :::::::: ::::::::
C;Genetics: A;Gene: GDB:CD22 A;Cross-references: GDB:127545; OMIM:107266	PKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQA . :
	798 ALHKRÓV
C;Keywords: alternative splicing; B-cell; cell adhesion; dimer; glycoprotein; phosphoprq F;1-19/Domain: signal sequence #status predicted <gig> F;20-847/Product: B lymphocyte cell adhesion protein #status predicted <mat></mat></gig>	Oy 632 DYAEVK 637 Db 841 DYVILK 846
F;346-399/Domain: immunoglobulin homology <imm1> F;609-661/Domain: immunoglobulin homology <imm2></imm2></imm1>	
F)688-706/Domain: transmembrane #stetus predicted <tra>. F)67,101,112,135,164,231,363,445,448,479,574,64/Binding site: carbohydrate (Asn) (coval F)764,789/Binding site: phosphate (Thr) (covalent) #status predicted</tra>	RESULT 11 850065 sialoadhesin - mouse
6%; Score 289.5; DB 2; Length 847; 0%; Pred. No. 3.1e-11;	change 09-Jul-2004
181; Conservative 116	: Willis, A.C.; Gordon, S
QY 1 MLLPLLISSLIGGSQAMDGRFWI-RVQESVWVPEGLCISVPCSFSYPRQ 48	A,Title: Sialoadhesin, a macrophage sialic acid binding receptor for haemopoietic cells v A,Reference number: S50065, MUID:95009950; PMID:7925291 A,Accession: S50065
QY 49 DWTGSTPAYGYWFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDA 108 :: : : :	A;Status: preilminary A;Molecule type: mRNA A;Residues: 1-1694 <cro> A;Cross-references: UNIPROT:Q62230; EMBL:Z36293; NID:g557253; PIDN:CAA85290.1; PID:g5572!</cro>
QY 109 QMQDESQYFFRVERG 123	Query Match 8.4%; Score 282.5; DB 2; Length 1694; Best Local Similarity 22.0%; Pred. No. 2.2e-10; Matches 135; Conservative 71; Mismatches 199; Indels 209; Gaps 21;
QY 124 SYVRYNFMNDGFELKVTVLSFTPRPQDHNTDLTCHV-DFSRKGV 166 120 YPICI, NILLECVPMPAAAVTSTSITTRSVFTRSELKFSPOWSHGKTVTCOLORADGKF, 229	QY 5 LLESSLIGGSQAMDGRFWIRYQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWFKAV 64
	Qy 65 TETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVERGS 124
Db 230 SNDTVQLNVKHTPKLEIKVTPSDAIVREGDSVTMTCEVSSSNPEYTTVSWLKDGTSLKKQ 289	Db 62 DYSGKRQVVIHSGDPKLVDKRFRGRAELMGNMDHKVCNLLLLKDLKPEDSGTYNFRFEISD 121
QY 191 NTPALE	Qy 125 YVRYNFWNDGFFLKVTVLSFTPRP
QY 215 RLLCAADSQP-PATLSWVLONRVLSSSHPWGPRPLGLELPGVKAGDSGRYTCRAE 268	QY 149
OY 269 NRLGSQORALDLSVQYPPENLRVMVSQANRTVLENLGNGTSLPVLEGGSLCLVCVTHS 326	Qy 175 RVAYAPRDLVISISRDNTPALEPQPQGNVPYLEAQKGGFLR- 215

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A;Accession: A344,A,A436,FL',438-449,Q',A51-502,A',503-792,X',794-908,R'
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A;Accession: A342,A',A',436,FL',438-449,Q',A',53242-3426,R',3428-3631,Q',3633-4A',Cross-references: EMBL:X62315, NID:G29469; PIDN:CA444373.1; PID:G29470
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A;Tille: Cloning of fuman heparan sulfate proteoglycan core protein, assignment of the g
A;Tille: Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additional and A; Additio
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A,Reference number: A40306, MUID:91365376, PMID:1679749
A,Accession: A40306
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A,Molecule type: mRNA
A,Residues: 'RT,892-908,'R',910-1101,'L',1103-1132,'L',1134-1221,'L',1223-1397 <KA2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  342 SPSQ------PSDPGV--LELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYSP 388
                                                                                                                                                                                  281
                                                                                                                                                                                                                                                                                                                                                                                                                                                       409 VRYPP-----LTPDLTTFLETQAGLVGI------LHCSVVSEPLATVVLSHGGLTL 453
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    -LLCAADSQP
                                                                                      294 FSAAWNDSGAYTCQATNDMGSLVSSPLSLHVFMAEVKNNPAGPVLENETVTLLCSTPKEA
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                                                                                                                                                                                                                                                                                                                                                                282 VQYPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVL
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574 YYCRTQAGPNTSGP 587
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A; Title: Matrix-associated heparan sulfate proteoglycan: core protein-specific monoclonal
A;Residues: 1018-1405,'G',1407-1409,'G',1411-1465 <DOD>
A;Cross-references: GB:M444283; NID:9184424; PIDN:AAA52699.1; PID:9184425
R;Heremans, A.; van der Schueren, B.; De Cock, B.; Paulsson, M.; Cassiman, J.J.; van den
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-21/Domain: signal sequence #status proteoglycan, glycoprotein, heparan sulfate, transmembing ;22-4391/Product: perlecan #status predicted <MAT>
;22-435/Domain: I <DOM1>
· 194-527/Domain: I <DOM1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298 RIVLENLGNGTSLPVLE----GQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLE 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                   shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F,4149-4151/Region: motor neuron attachment (L-R-E) motif
F;4299-4401/Region: motor neuron attachment (L-R-E) motif
F;6571,76/Bainding site: heparan sulfate (Ser) (covalent) #status predicted
F;85,554,1755,2121,3072,3105,3279,3780,3836,4068/Binding site: carbohydrate
F;2995,3933,4179/Binding site: chondroitin sulfate (Ser) (covalent) #status |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 MNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVISISRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 NTPALEPOPOGNVPYLEAQKGOFLRILCAADSOPPATLSWVLQNRVLSSSHPWGPRPLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3338 SLPGRATARNELLHFERAAPEDSGRYRCRVTNKVGSAEAFAQLLVQGPPGSLPATSIPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGRFWIRVQESVMVPEGLCISVPCSFSYPRQD--WT--GSTPA----YGYW----
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ilarity 21.1%; Pred. No. 4.5e-08;
Conservative 53; Mismatches 197; Indels 220;
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;Residues: 2166-2171,'X',2173-2175,'X',2177-2185 <HE3>
;Note: peptide potentially matches four different regions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homology
homology
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repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <EG7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;2007-2034/Domain: transmembrane #status predicted <TRM>;3687-4391/Domain: V <DOMS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1159-1206/Pomain: laminin-type EGF-like homology <LEG>1563-1610/Domain: laminin-type EGF-like homology <EG7>1613-1668/Domain: laminin-type EGF-like homology <LEG8
                                                                                                                                                                                                           A; Reference number: A33625; MUID: 90078352; PMID: 2687294
                                                                                                                                                                                                                                                                               Molecule type: protein
Residues: 1379-1384,'X',1386-1388,'X',1390-1398 <HE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat |
repeat |
repeat |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;3845-3880/Domain: EGF homology <EGF1>
F;3888-3921/Domain: EGF homology <EGF>
F;3854-4106/Domain: laminin G repeat homology <LG2>
F;4147-4175/Domain: EGF homology <EGF2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199-234/Domain: II <DOM2>
199-234/Domain: LDL receptor ligand-binding
1265-319/Domain: LDL receptor ligand-binding
1325-359/Domain: LDL receptor ligand-binding
1366-403/Domain: LDL receptor ligand-binding
1531-1676/Domain: III <DOM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Map position: 1p36.1-1p36.1
C,Keywords: chondroitin sulfate proteoglycan;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDB:126372; OMIM:142461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3277 ----ICNATSPAGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1677-3686/Domain: IV < DOM4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 126; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Cross-references:
                                                                                                                                                                                                                                               Accession: B33625
                                                                                                                                                                                                                                                                                                                                               Accession: A33625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: GDB: HSPG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
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Db 391 TPALRWTKDSTPLGDGPMLSLSSITFDSNGTYVCEASLPTVPVLSRTQNFTLLVQ 445 Qy 386 YSPKLLGPSCSW-EAEGLHGSCSSQASPAPSLRWMLGEELLEGNSSQDSFEVTP 438	RESULT 14 A35664 B-6618 adhesion p C; Species: Homo s C; Species: Homo s C; Cession: A356 C; Accession: A356 C; Accession: A356 A; Title: The Taylor and the A; Residues: 1-647 A; Title: The Taylor and A; Residues: 1-647 A; Traces reference C; Genetics: A; Residues: 1-647 A; Residues: 1-647 A; Residues: 1-647 A; Coss-reference C; Genetics: C; Genetics: A; Gonetics: C; Genetics:	
Db 3398 STPTVQVTPQLETKSIGASVEPHCAVPSDQGTQLRWFKEGGQLPPGHSVQDGVLR 3452 Qy 354 LPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHXSPKILGPSCSWEAEG 401 Db 3453 IQNLDQSCQGTYICQAHGPWGKAQASAQLVIQALPSVLINIRTSVQTVVVGHAVEFE 3509 QY 402 LHCSCSSQASPAPSLRWWLGEELLEGNSSQDSFEVTPSSAGPWANSSLSLHGG 454 Db 3510CLALGDPKPQVTWSKVGGHLRPGIVQSGGVVRIAHV 3545 QY 455 -LSSGIRLRCEAMNVHGAQSGSILQLPDKKGLISTAFSNGAFLGIGITALLFLCLA 509 1546 ELADAGQYRCTATNAAGTTQSHVLLLVQALPQISMEQEVRVPAGSAAVPPCIA 3598	RESULT 13 RESULT	

279 Db 391 TPALRWTKDSTPLGDGFN 409 Qy 386 YSPKLLGPSCSW-EAEC	Search completed: November 5, 2004, 13:51:06 Job time: 22.7654 secs 09-Jul-2004	<pre>Garin-Chesa, P.; Rettig, W.J :otein of epithelial cancers: ;; PIDN:CAA56327.1; PID:g5351</pre>	215; Gaps 38; TPAYGY-WFKA 63 	DAQMQDESQ 115 SEASYGDERD 122 130 SENGNPAPK 182	INTDLTCHVDFS 162	
237LESSHPWGPRPLGLELPGUKAGDSGRYTCRAENRLG-SQQRALD 350 LQCDFSSSHPKEVQFFERNGLLGKESQLNFDSISPEDAGSYSCWNNSIGGASIAT 280 LSVQYPENLRWWSGNRTULENLGNGTSLPVLEGGSLCUVCYTHSSPPARLSWT 410 LEVLYAPPRLAVSMSPGDQVWRGGSATLTCESDANPPVSHYTWPDWN 336 QRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSL6-LSVHYSPKLLGPS	sion 12-Aug-1996 #text_change	"Adjacer Res. 54, 5761-5765, 1994 "Adjacer Res. 54, 5761-5765, 1994 "Ajfitle: Molecular cloning of the B-CAM cell surface glycoprotein A, Reference number: 137202, MulD:95042297, PMID:7954395 A, Accession: 137202 A, Accession: 137202 A, Molecule type: mRNA A, Residues: preliminary; translated from GB/EMBL/DDBJ A, Molecule type: mRNA A, Residues: 1-588 A, Cross-references: UNIPROT:P50895; EMBL:X80026; NID:g535178; PIDI A, Gross-references: UNIPROT:P50895; EMBL:X80026; NID:g535178; PIDI A, Gross-references: UNIPROT:P50895; EMBL:X80026; NID:g535178; PIDI A, Gross-Residues: B-CAM	Query Match 7.1%; Score 239.5; DB 2; Length 588; Best Local Similarity 23.1%; Pred. No. 3.8e-08; Matches 155; Conservative 78; Mismatches 223; Indels 215; Gaps 5 LLLSSLLGGSQAMDGRFWIRVQESVMVPBGLCISVPCSFSYPRQDWTGSTPAYGY-WFKA 5 LLLSSLLGGSQAMDGRFWIRVQESVMVPBGLCISVPCSFSYPRQDWTGSTPAYGY-WFKA 17 LLLAVLLAAHPDAQAEVRLSVPPLVEVMRGKSVILDCTPTGTHDHYMLEWF	64 VTETIKGAPVAINHQSREVEMSTRGRFQLIGDPAKGNCSLVIRDAQMQDESQ :	131RPODBHNTDLTCHUDES 183 ITWYRNGQRLEVPVEMNPEGYMTSRTVREASGLLSLTSTLYLPCRKDDRDASFHCAAHYS 163RKGVSAQRTVRLKVAYAPRDLVISISRDNTPALEPQFGGNVFYLEAGKGGFLRLC 163RKGVSAQRTVRLHYPTEHVQFWVGSPSTPA	

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November 5, 2004, 13:53:32; Search time 109.924 Seconds (without alignments) 2053.348 Million cell updates/sec
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3377
1 MLPILLSSLLGGSQAMDGR......RPEARMPKGTQADYAEVKFQ 639
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1: /cgn2_6/ptodata/2/pubpaa/PCT_PUBCCMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_BM PUB.pep:*

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 28, Appl	Sequence 33, Appl	Sequence 33, Appl	Sequence 28, Appl	Sequence 149, App	Sequence 7, Appli	Sequence 10, Appl	Sequence 9, Appli	Sequence 8, Appli	Sequence 259, App	Sequence 259, App	Sequence 259, App	Seguence 259, App
DI	US-10-158-238-28	US-09-984-130-33	US-09-836-353A-33	US-09-910-600-28	US-09-984-130-149	US-10-403-938-7	US-10-614-853-10	US-09-910-600-9	US-09-910-600-8	US-09-978-295A-259	US-09-978-697-259	US-09-978-192A-259	US-09-999-832A-259
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-09-978-189-25	-09-978-608A-25	US-09-978-585A-259	-09-978-191A-25	-09-978-403A-25	-09-978-564A-25	-09-999-833A-25	-09-981-915A-2	-09-978-824-25	09-918-585A-2	-09-999-834A-25	-09-978-423A-25	-09-978-193A-25	-09-999-830A-25	-09-978-757A-25	-09-978-187B-25	09-978-643A-2	-09-978-375A-25	09-978-298A-25	-09-978-188A-25	-09-978-681A-25	-09-978-194A-25	-09-999-829A-25	-978-299A-25	-09-978-544A-25	-09-978-665A-25	-09-978-802A-25	09-999-831A-25	-10-052-586-11	-10-174-590-11	-10-176-758-11	US-10-175-737-118
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ALIGNMENTS

RESULT 1 US-10-158-238-28 Squares 28, Application US/10158238 Squares 28, Application US/10158238 CENERAL INFORMATION: APPLICANT: Immunex Corporation APPLICANT: Dirk, Anderson M. APPLICANT: Marken, John S. TITLE OF INVENTION: SIGLEC-12 POLYNDCLEOTIDES, AND METHODS OF USE THEREC FILES OF INVENTION: SIGLEC-12 POLYNDCLEOTIDES, AND METHODS OF USE THEREC CURRENT FILING DATE: 2002-05-29 CURRENT FILING DATE: 2001-05-29 PRIOR PAPLICATION NUMBER: US 60/294,199 PRIOR FILING DATE: 2001-05-29 NUMBER OF SEQ ID NOS: 30 SOFTWARE: Patentin version 3.1 SEQ ID NO 28 LENGTH: 639 TYPE: PRT CORGANISM: Home sapiens US-10-158-238-28	Query Match Best Local Similarity 100.0%; Pred. No. 2e-221; Matches 639; Conservative 0; Mismatches 0; Indels' 0; Gaps 0;	1 MLIPLLISSLIGGSQAMDGRFWIRVQESYMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW 60	61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQNQDESGYFFRV 120 	121 BRGSYVRYNFWNDGFFLKVTVLSFTPRPODHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP 180
RESULT 1 US-10-158 Sequence Publical GENERALI APPLICA APPLICA APPLICA APPLICA APPLICA APPLICA APPLICA PRICE N CURREN PRICE N PRICE ery Ma Best Loc Matches	රු අ	P S	à	

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FKAVTETTKGAPVATNHOSREVEMSTRGRFOLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120
                                                                                                                                                                                                                                                                   241 HPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVWVSQANRTV 300
                                                                                                                                                                                                                                                                                                                                                                         301 LENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVE 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 HEGEFTCHARHPLGSQHVSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPAPSLRWWL 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYI 540
                                                                                                                                                                                                                                                                                                                                                                                                                         301 LENLGNGTSLPVLEGOSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVE 360
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Publication No. US20030129885A1
GENERAL INFORMATION: US2003129885A1
TITLE REPERRICE TO INVESTION: 12 Human Secreted Proteins
FILE REPERRICE: PF4997
CURRENT FILING DATE: 2001-04-18
PRIOR PILING DATE: 2000-04-19
PRIOR PLING DATE: 2000-04-19
PRIOR FILING DATE: 1999-10-27
PRIOR FILING DATE: 1999-10-27
PRIOR FILING DATE: 1999-10-27
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Pred. No. 7.5e-220;
0; Mismatches 3;
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Best Local Similarity 99.5%;
Matches 636; Conservative
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SEQ ID NO 33
LENGTH: 639
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Pred. No. 7.5e-220;
0; Mismatches 3;
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TITLE OF INVENTION: 12 Human Secreted Proteins
FILE REPERENCE: PF48929
CURRENT APPLICATION NUMBER: US/09/984,130
CURRENT PILING DATE: 2001-10-29
PRIOR PILING DATE: 2000-10-30
PRIOR PELING DATE: 2000-10-30
PRIOR PILING DATE: 2000-10-30
PRIOR PILING DATE: 2000-04-18
PRIOR PILING DATE: 2000-04-19
PRIOR APPLICATION NUMBER: 60/198,407
PRIOR APPLICATION NUMBER: PCT/US99/25031
PRIOR APPLICATION NUMBER: 60/105,971
PRIOR APPLICATION NUMBER: 60/105,971
PRIOR APPLICATION NUMBER: 60/105,971
PRIOR APPLICATION NUMBER: 60/105,971
PRIOR APPLICATION NUMBER: 60/105,971
PRIOR APPLICATION NUMBER: 60/105,971
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Best Local Similarity 99.5%;
Matches 636; Conservative
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SEQ ID NO 33
LENGTH: 639
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ORGANISM: Homo sapiens
US-09-984-130-33
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Pred. No. 1.9e-218;
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US-09-984-130-149

Sequence 149, Application US/09984130

Publication No. US20030055231A1

GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENDITON: 12 Human Secreted Protein
FILIE REPERNCE: PF499P2

CURRENT APPLICATION NUMBER: US/09/984,130

CURRENT FILING DATE: 2001-10-29

PRIOR FILING DATE: 2001-0-30

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-04-18

PRIOR FILING DATE: 2000-04-19

PRIOR FILING DATE: 1999-10-27

PRIOR FILING DATE: 1999-10-27

PRIOR FILING DATE: 1999-10-27

PRIOR FILING DATE: 1999-10-27

PRIOR FILING DATE: 1999-10-27

PRIOR FILING DATE: 1999-10-28

NUMBER OF SEQ ID NOS: 149

SOFTWARE: PATCHING DATE: 1998-10-28

NUMBER OF SEQ ID NOS: 149

LENGTH: 697
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CORGANISM: Homo sapiens
US-09-984-130-149
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                                                                                       ERGSYVRYNFMNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP 180
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      PKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: L3-995-2
US-09-910-600-28
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US-09-910-600-28
US-09-910-600-28
Sequence 28, Application US/09910600
Publication No. US20030036631A1
GENERAL INFORMATION:
APPLICANT: Longphre, Malinda
APPLICANT: Longphre, Malinda
TITLE OF INVENTION: NOVEL SIGLECS AND USES THE
FILE PEPERENCE: DOORNP
CURRENT APPLICATION NUMBER: US/09/910,600
CURRENT FILING DATE: 2001-07-20
PRIOR FILING DATE: 2001-07-21
NUMBER OF SEQ ID NOS: 32
SOFWWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 697
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ORGANISM: Artificial Sequence
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Matches

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Query Match

LENGTH: 697

US-10-403-938-7

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61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120
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APPLICANT: WILLIAM WOOD
APPLICANT: WILLIAM WOOD
APPLICANT: THOMAS WU
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE
TITLE OF INVENTION: RELATED DISEASES
FILE REFERENCE: P1973R1-US
                                                                                                                      1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
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                                                                       1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
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Pred. No. 1.9e-218;
                            0; Mismatches
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CURRENT FILING DATE: 2003-07-08
PRIOR APPLICATION NUMBER: US 60/394,485
PRIOR FILING DATE: 2002-07-08
NUMBER OF SEQ ID NOS: 28
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KATHRYN DENNIS
SHERMAN FONG
                            Matches 638; Conservative
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APPLICANT: HENRY CHIU
Best Local Similarity
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Publication No. US20040025195A1

GENERAL INFORMATION:

APPLICANT: Britsol-Myers Squibb Company

TITLE OF INVENTION:

TITLE OF INVENTION:

EGS-19

TITLE OF INVENTION:

EGS-19

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER:

CURRENT FILING DATE:

2003-03-28

NUMBER OF SEQ ID NOS:

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ORGANISM: Homo sapiens
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                                                                                                                                                PKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120
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                                                                                                                 -----VLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
                                                                                                                                                                                                                                                       181 TGAALSSQGTKPTTSHFSVLSFTPRPQDHNTDLTCHVDFSRKGVSVQRTVRLKVAYAPRD
                                                                                                                                                                                                                                                                                                     241 LVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP
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                                                                                                     MLLPLILSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
                                                                              Gaps
                                                                              Indels 58;
                                                       Length 697;
                                                                                                                                                                                             ERGSYVRYNFMNDGFFLKVT--------
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                                                     Score 3334; DB 16;
Pred. No. 1.9e-218;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/09910600
; Publication No. US20030036631A1
; GENERAL INFORMATION:
; APPLICANT: Longphre, Malinda
; APPLICANT: Chang, Han
APPLICANT: Whitney, Gena
; TITLE REPERENCE: DO003NP
; CURRENT APPLICATION NUMBER: US/09/910,600
; CURRENT FILING DATE: 2001-07-20
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 32
                                                       Query Match
Best Local Similarity 91.5%;
Matches 638; Conservative
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-614-853-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      378 VSLSLSVHYSPXLLGPSCSWEAEGLHCSCSSQASPAPSLRWWLGEELLEGNSSQDSFEVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWFKAVTETTKGAPVATNH
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                                                                                                                                                                                                                                                                                                     Query Match 97.7%; Score 3299; DB 10; Best Local Similarity 100.0%; Pred. No. 4e-216; Matches 622; Conservative 0; Mismatches 0;
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; SEQ ID NO 9
; LENGTH: 622
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-910-600-9
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US-09-910-600-8
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APPLICATION NUMBER:
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                      95; Gaps
                                                                                                                                                                                   DB 10; Length 544;
                                                                                                                                                                                Score 2803.5; DB 10; Lengthered. No. 1.9e-182; 0; Mismatches 0; Indels
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Grimaldi, J. Christopher
                                                                                                                                                                                83.0%;
85.1%;
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Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
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Desnoyers, Luc
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                                                                                                                                                                                                                                 Matches 544; Conservative
LENGTH: 544
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                             Query Match
Best Local Similarity
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A APPLICANT: Kijavin, Yvarich J
A PRICANT: Kijavin, Yvarich J
A PRICANT: Kijavin, Yvar A.
A PRICANT: Sijavin, Yvar A.
A PRICANT: Sijavin, Yvar A.
A PRICANT: Sijavin, Yvar A.
A PRICANT: Silavin, Jane P.
A PRICANT: Silavin, Jane P.
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A PRICANT: Silavin, Jane J.
A PRICANT: Silavin, Jane J
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60/08019

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241 HPWGPRPLGLELPGVKAGDSGRYTCRAENRIGSQQRALDLSVQYPPENLRVMVSQANRTV 300 121 ERGSYVRYNFMNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP 180 RDLVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSS 240 LENIGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVE 360 361 HEGEFTCHARHPLGSQHVSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPAPSLRWWL 420 GEELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGSILQLP 480 1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW 1 MILPILLESILGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWIGSTPAYGYW Gaps 95; Length 544; 2; Indels 361 HEGEFTCHARHPLGSQHVSLSLSVHY--------Query Match
82.6%; Score 2790.5; DB 9;
Best Local Similarity 84.8%; Pred. No. 1.5e-181;
Matches 542; Conservative 0; Mismatches 2; 1 RELING DATE: 1998-06-06

RAPPLICATION NUMBER: 60/084637

RAPLICATION NUMBER: 60/084639

RAPLICATION NUMBER: 60/084640

RAPLICATION NUMBER: 60/084640

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RAPLICATION NUMBER: 60/084600

RELING DATE: 1998-05-07

RAPLICATION NUMBER: 60/084627

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RAPLICATION NUMBER: 60/084633

RAPLICATION NUMBER: 60/08538

RAPLICATION NUMBER: 60/085339

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PPLICANT: Wood, William I.
THE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
THE OF INVENTION: Acids Encoding the Same
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CURRENT FILING DATE: 2001-10-16
                                                                                                                                                                                                                                                                                     Sequence 259, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
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Gurney, Austin L.
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PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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APPLICATION NUMBER: 60/064249
FILING DATE: 1997-11-03
APPLICATION NUMBER: 60/065311
FILING DATE: 1997-11-13
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FILING DATE: 1997-11-21
APPLICATION NUMBER: 60/077450
FILING DATE: 1998-03-10
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APPLICATION NUMBER: 60/077641
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Pov. Margaret Ann
Povid L.
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Filvaroff, Ellen
Fong, Sherman
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Goddard, Audrey
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                                                                                                                                                                                                                                                                                                                                                                                    Botstein, David
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                                                                                                                                                                                                                                                                                                                                                                                                        Desnoyers, Luc
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APPLICANT: Baker Kevin P.
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APPLICATION NUMBER: 60/078910
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APPLICATION NUMBER: 60/078936
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APPLICATION NUMBER: 60/079294
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LING DATE: 1998-03-27
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APPLICATION NUMBER: 60/079923
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APPLICATION NUMBER: 60/081195
FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081203
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PRIOR APPLICATION NUMBER: 60/081952
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PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
                                                                                                     60/078939
                                                                                                                                                                                    LICATION NUMBER: 60/079656
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PLICATION NUMBER: 60/079664
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APPLICATION NUMBER: 60/080327
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LICATION NUMBER: 60/080328
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APPLICATION NUMBER: 60/080333
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                                         1998-03-20
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APPLICATION NUMBER: 60
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1 MILPILLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAXGYW

1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW

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481 DKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYI

387

601 QESQEELHYATLNFPGVRPRPRARMPKGTQADYAEVKFQ 639 OESQEELHYATLNFPGVRPRPBARMPKGTQADYAEVKFQ 544

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361 HEGEFTCHARHPLGSQHVSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPAPSLRWWL 420

361 HEGEFTCHARHPLGSQHVSLSLSVHY------

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301 LENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVE

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421 GEELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGSILQLP 480

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181 RDLVISISRDNTPALEPOPOGNVPYLEAGKGOFLRLLCAADSOPPATLSWVLQNRVLSSS

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Sequence 229, Application US/09978192A
Parent No. US20020177553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Barker Kevin P.
APPLICANT: Borstein, David
APPLICANT: Bestoin, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Ferrara, Napoleon
APPLICANT: Food, Sherman
APPLICANT: Food, Sherman
APPLICANT: Gao, Wei-Olang
APPLICANT: Goo, Wei-Olang
APPLICANT: Geober, Hanspeter Fong, Sherman
Gao, Wel-Oiang
Garo, Wel-Oiang
Gerritsen, Mary E.
Goddward, Audrey
Grimaldi, J. Christopher
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Grimaldi, Nary A.
Pan, James;
Paoni, Nicholas F. RESULT 12 US-09-978-192A-259 APPLICANT: APPLICANT: APPLICANT: APPLICANT:
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Length 544;

Score 2790.5; DB 9; Pred. No. 1.5e-181;

82.6%;

Query Match Best Local Similarity

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FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/081070
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FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081071
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FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081229
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APPLICATION NUMBER: 60/081819
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APPLICATION NUMBER: 60/081195
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FILING DATE: 1998-04-15
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ICATION NUMBER: 60/082700
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APPLICATION NUMBER: 60/083559
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FILING DATE: 1998-04-
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FILING DATE: 1998-05
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                                                                      APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                           FILE REFERENCE: P2630PIC9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/077450
FILING DATE: 1998-01-10
APPLICATION NUMBER: 60/077450
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PRIOR APPLICATION NUMBER: 60/064249
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APPLICATION NUMBER: 60/065311
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APPLICATION NUMBER: 60/066364
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PRIOR FILING DATE: 1998-03-20
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FILING DATE: 1998-03-20
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PRIOR FILING DATE: 1998-03-26
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PRIOR FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/079786
FILING DATE: 1998-03-27
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FILING DATE: 1998-03-30
APPLICATION NUMBER: 60/080105
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APPLICATION NUMBER: 60/080333
FILING DATE: 1998-04-01
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FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/080194
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Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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                                                        umas, Daniel
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APPLICANT: Tunas, P. Mickey
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REPERBNCE: P2630P1628
CURRENT APPLICATION NUMBER: 09/91885
PRIOR APPLICATION NUMBER: 09/91885
PRIOR FILING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-12
PRIOR PLING DATE: 1998-03-10
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   446 NVVPTAGPLAQKRNQKATPNSPRTPPPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPES 505
                                                                                                                            506 QESQEELHYATINFPGVRPRPEARMPKGTQADYAEVKFQ
                                                                  601 QESQEELHYATINFPGVRPRPEARMPKGTQADYAEVKFQ
                                                                                                                                                                                                                                                                     Sequence 259, Application US/09999832A Publication No. US20020192706A1 GENERAL INFORMATION:
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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APPLICATION NUMBER: 60/078910
FILING DATE: 1998-03-20
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Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Gerritsen, Mary E
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Filvaroff, Ellen
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
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Kuo, Sophia S.
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Eaton, Dan
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Pred. No. 1.5
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/08459
PRIOR PILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-05-07
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R FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/082568
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                ICATION NUMBER: 60/079294
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                                                              ERGSYVRYNFWNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP 180
                                                                                                  ERGSYVTYNEMNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP 180
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                      PKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120
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Publication No. US20030004102A1
GENERAL INFORMATION:
APPLICANT: Baker Kevin P.
APPLICANT: Bater Kevin P.
APPLICANT: Bater Kevin P.
APPLICANT: Baten, Dan
APPLICANT: Firsta, Napoleon
APPLICANT: Firsta, Napoleon
APPLICANT: Firsta, Napoleon
APPLICANT: Firsta, Mapoleon
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gedard, Audrey
APPLICANT: Gedard, Austin L.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Hillan, Kanneth J
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Navin Sophia S.
APPLICANT: Navin Sophia S.
APPLICANT: Navin Mary A.
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Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Williams, P. Mickey
Wood, William I.
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TITLE OF INVENTION: Acids Encoding the Same CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT PELLING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 09/04249
PRIOR APPLICATION NUMBER: 06/062250
PRIOR PELLING DATE: 1207-10-17
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R APPLICATION NUMBER: 60/082569

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FILING DATE: 1998-04-22
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APPLICANT: Paoni, Nicholas F.
APPLICANT: Stewart, Timothy A.
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APPLICANT: Tumas, Daniel
APPLICANT: William: P. Mickey
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Geritsen, Mary E.
Goddard, Audrey,
Goddwski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kujavin, Ivar J
Kujavin, Ivar J
Kujavin, Ivar J
Rujer, Mary A.
RESULT 15
US-09-978-608A-259
Sequence 259, Application US/09978608A
Publication No. US20030045462A1
GENERAL INFORMATION:
                                                                                                                                                                                                               APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bottein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan
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US-09-978-608A-259
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420	386	480	386	540	445	009	505		
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Search completed: November 5, 2004, 14:13:49 Job time : 112.924 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 5, 2004, 13:50:18; Search time 140.458 Seconds (without alignments) 2617.614 Million cell updates/sec Run on:

US-09-937-636-4 3377 1 MLLPILLSSLLGGSQAMDGR.....RPEARMPKGTQADYAEVKFQ 639

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 seqs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Q961c7 homo sapien	Qeuxis homo sapien	Aag88703 homo sapi	Q96rl6 homo sapien	Bac85493 homo sapi	ยาพ	Q8by18 mus musculu	O15389 homo sapien	σ	mus			homo	homo	pan	Q6pj50 mus musculu	4	Aag72479 mus muscu	Aah23280 mus muscu	արց ա	homo	Q6gtu4 homo sapien	homo	OMOL	Aaq88735 homo sapi	Q8bu57 mus musculu	043699 homo sapien	ഥ	٠.	P07722 rattus norv	P20917 mus musculu
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Yillalon D.K., Muzny D.M., Sodergren E.J., Lu K., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Granstein J. M., Mares R.M., Macherich A., Schein J.E., Jones S.J.M., Mares R.M., Porner A.S., Schein J.E., Jones S.J.M., Mares R.M., Porner M. Schein J.E., Jones S.J.M., Mares R.M., Porner M. Schein J.E., Jones S.J.M., Mares R.M., Porner M. Schein J.E., Jones S.J.M., Mares R.M., Porner M. Schein J.E., Jones S.J.M., Mares R.M., Porner M. Schein J.E., Jones S.J.M., Mares R.M., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Porner M. P., Po
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masked by cis interactions with sialic acids on the same cell surface. In the immune response, may act as an inhibitory receptor upon ligand induced tyrosine phosphorylation by recruiting cytoplasmic phosphatase(s) via their SH2 domain(s) that block signal transduction through dephosphorylation of signaling molecules. -1- FUNCTION: Putative adhesion molecule that mediates sialic-acid dependent binding to cells. Preferentially binds to alpha2,3- or 2,6-linked sialic acid. The sialic acid recognition site may be

SUBUNIT: Interacts with PTPN6/SHP-1 upon phosphorylation.
SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1-4);
secreted (isoform 5).
ALTERNATIVE PRODUCTS:

Event=Alternative splicing, Named isoforms=5; Name=1; Synonyms=Long; IsoId=Q96LC7-1; Sequence=Displayed;

Name=2; Synonyms=Short, Sv1; IsoId=Q96LC7-2; Sequence=VSP_002565;

Name=3; Synonyms=Sv3; IsoId=Q96LC7-3; Sequence=VSP_002564; Name=4; Synonyms=Sv4;

IsoId=Q96LC7-4; Sequence=VSP_002561;

Name=5; Synonyms=8v2;

IsoId=096LC7-5; Sequence=vSP 002562, VSP 002563;

IsoId=096LC7-5; Sequence=vSP 002562, VSP 002563;

IsoId=096LC7-5; Sequence=vSP 002562, VSP 002563;

IsoId=096LC7-5; Sequence=vSP 002562, VSP 002563;

(eosinophils, monocytes and natural killer cell subpopulation).

Isoform 5 is found to be the most abundant isoform. Pound in lymph node, lung, ovary and appendix. Isoform 1 is found at high levels and isoform 2 at lower levels in bone marrow, spleen and spinal chord. Isoform 2 is also found in brain. Isoform 4 is specifically cound in natural killer cells.

-!- DOMAN: Contains 1 copy of a cytoplasmic motif that is referred to as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in modulation of cellular responses. The phosphorylated TIM modulation of cellular responses. The phosphorylation of Tyr-667 is involved in binding to PTPN6.
-!- PTM: Phosphorylation of Tyr-667 is involved in binding to PTPN6.
-!- PTM: Phosphorylation 3 immunoglobulin superfamily. SIGLBC (slalic acid binding Ig-like lectin) family.
-!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domains.

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EMBL; AY029277; AAK40255.1; -Q9Y286; 107S EMBL; EMBL; HSSP; EMBL;

----VLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 182

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oe. 5. 3. adhesion; Glycoprotein; in; Phosphorylation; Repeat; Signal;	Potential. Sialic acid binding Ig-like lectin 10. Extracellular (Potential). Potential. Cytoplasmic (Potential). Ig-like V-type. Ig-like C2-type 1. Ig-like C2-type 2. Ig-like C2-type 3.	ITIM motif 2. By similarity. By similarity. By similarity. By similarity. By similarity. By similarity. Phosphotyrosine. N-linked (Glounc) (Potential). N-linked (Glounc) (Potential). N-linked (Glounc) (Potential). N-linked (Glounc) (Potential). N-linked (Glounc) (Potential). N-linked (Glounc) (Potential). Missing (in isoform 4).	/FTIG=VSP 002251. TALTOKPOVYIPETLEPGOPVTVICVFNWAPEECPPPSFSW TGAAL -> TGMRWGCNPCLSHWGGTLGTAYGLSREGSQPP LQHYNLPPSESLSQP (in isoform 5). FTIG=VSP 002562. Missing (in isoform 5). FTIG=VSP 002563. Missing (in isoform 3). FTIG=VSP 002564. Missing (in isoform 2). FTIG=VSP 002565. Y-FT Abolishes binding to PTPN6. S -> P (in Ref. 4). Y -> A (in Ref. 4). P -> S (in Ref. 3). L -> P (in Ref. 3). L -> P (in Ref. 3). L -> P (in Ref. 3). L -> P (in Ref. 3).	
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PubMed=12975309;
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Clark H.F., Gurney A.L., Crowley C., Currell B., Deuel B., Dowd
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd
Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
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PS00290; IG_MHC; UNKNOWN 1.
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82.6%; Score 2790.5; DB 2
Best Local Similarity 84.8%; Pred. No. 4.4e-168;
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                                                                                                                                                                                                                                                                 362
                                                                                                                                                                                                                                                                                        GEFTCHARHPLGSQHVSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPAPSLRWWLGE 422
                                                                                                                                                                                                                                                                                                                                                                                                            480
     TGAALSSQGTKPTTSHFSVLSFTPRPQDHNTDLTCHVDFSRKGVSVQRTVRLRVAYAPRD 240
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                                                                                                                                                                    WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           601 VPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNOKKQYQLPSFPEPKSSTQAPESQE
                                                                                                                                                                                                                                                                      NLGNGTSLPVLEGOSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE
                                                                                                                                                                                                                                                                                                                                                                                                            GEFTCHARHPLGSQHVSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPAPSLRWWLGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGS1LQLPDK
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Bioinformatics assessment.";

Genome Res. 13:2265-2270(2003).

EMBL; AY358337; AAQ86703.1; -...

InterPro; IPR003599; Ig.

InterPro; IPR003598; Ig-like.

InterPro; IPR003006; Ig-like.

InterPro; IPR003006; Ig-mHC.

Pfam, PF00047; Ig; 2.

SMART; SM00409; IG; 3.

SMART; SM00409; IGc; 2.
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MEDLINE=2288796; PubMed=12975309;

Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,

Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,

Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd E Eaton D., Foster T., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,

Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,

Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,

Godowski P.,
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Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, E
Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
NCBI_TAXID=9606;
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Last sequence update)
Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
SIGLECLO.
ORFNames=UNQ477;
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Butheria; Primates; Catarrhini; Hominidae; Homo
                                     NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 FKAVIETIKGAPVAINHQSREVEMSIRGREQLIGDPAKGNCSLVIRDAQMQDESQYFFRV
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Effort to Identify Novel Human Secreted and Transmembrane Proteins:
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 45, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Sialic acid binding Ig-like lectin 11 precursor (Siglec-11) (Sialic acid-binding lectin 11) (UNQ9222/PRO28718).
Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Sebragiri S., Simmons L., Singh J., Smith V., Shinson J., Vagta A. Wandlen R., Watenabe C., Wieand D., Woods K., Xie M.H., Yansura Yi. S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 2790.5; DB 2; Length 544;
Pred. No. 4.4e-168;
0; Mismatches 2; Indels 95:
                                                                                                                                                                                                                                                                                                                                        Entiformatics Assessment.";
Genome Res. 13:2265-2270(2003).
EMBL; AY359337; AAQ88703.1; -.
SEQUENCE 544 AA; 60267 MW; 4DA4E1EFD60AC8CB CRC64;
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Best Local Similarity 84.8%; P
Matches 542; Conservative 0;
MLPLLLSSLLGGSQANDGRF
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Homo sapiens (Human). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bioinformatics assessment...;
Genome Res. 13.265-2270(2003).
-! FUNCTION: Putative adhesion molecule that mediates sialic-acid dependent binding to cells. Preferentially binds to alpha2.8-
linked sialic acid. The sialic acid recognition site may be masked by cis interactions with sialic acids on the same cell surface. In the immune response, may act as an inhibitory receptor upon ligand induced tyrosine phosphorylation by recruiting cytoplasmic phosphorses(s) via their SNE domain(s) that block signal transduction through dephosphorylation of signaling molecules.
-! SUBUNIT: Interacts with PTPN6/SHP-1 and PTPN11/SHP-2 upon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=096RL6-2; Sequence=VSP 008764;
-!- TISSUE SPECIFICITY: Expressed by macrophages in various tissues including Kupffer cells. Also found in brain microglia.
-!- DOWAIN: Contains I copy of cytoplasmic motif that is referred to as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in modulation of cellular responses. The phosphorylated ITIM motif can bind the SH2 domain of several SH2-
                                                                      PTPN11.
                                                                                                                                                                                                                                                                           MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Chow B., Chui C., Crowley C., Curzell B., Dowd P.,
Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
Godowski P., Gray A.;
"The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins: a
                                                                                                                                                         "Cloning and characterization of human Siglec-11. A recently evolved signaling that can interact with SHP-1 and SHP-2 and is expressed by tissue macrophages, including brain microglia."; J. Biol. Chem. 277:24466-24474(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PTM: Phosphorylated on tyrosine residues.
-!- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC (sialic acid binding 19-like lectin) family.
-!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                 SEQUENCE FROM N.A. (ISOFORM 1), AND INTERACTION WITH PTPN6 AND MEDLINE=22086217; Pubmed=11986327; DOI=10.1074/jbc.M202833200; Angata T., Kerr S.C., Greaves D.R., Varki N.M., Crocker P.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphorylation.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q96RL6-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 containing phosphatases.
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FOLTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYVRYNFMNDGFFLKVTVLSFTPRPQ 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     330 ARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYSPK 389
                                                                                                                                                                                                                                                                                                                                                                                    02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last Sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last sequence to the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contr
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                                              KGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINV
                                                                                                                           VPTAGPLAQKKNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPESQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 MVPEGLCISVPCSFSYPRODWTGSTPAYGYWFKAVTETTKGAPVATNHQSREVEMSTRGR
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Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
Pukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
Pukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
Yamashita H., Mateuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda J.
Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima J.
Masuho Y., Nagai K., Isogai T.;
"NEDO human cDNA sequencing project.";
Submitted (JUL-2003) to the BMEL/GenBank/DDBJ databases.

EMBL; AK122619; BAC85493.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primata, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Pred. No. 4e-125;
1; Mismatches 3; Indels
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                                                                                                                                                                                                        SQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK 637
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Best Local Similarity 69.0
Matches 421; Conservative
                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Human)
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Homo sapiens (F
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122 ERGSRVRHSFLSNAFFLKVTALTKKPDVYIPETLEPGQPVTVICVFNWAFKKCPAPSFSW 181
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GNSSQGSFEUTPSSAGPWANSSLSLHGGLSSGLRLRCKAWN
VHGAQSGSVFQLLPG -> W (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 TGAALSPRRTRPSTSHFSVLSFTPSPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEFTCHAQHPLGSQHVSLSLSVHYPPQLLGPSCSWEAEGLHCSCSSQASPAPSLRWWLGE
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                                                                                                                               11.
                                                                                                                                                                                                    Ig-like V-type.

Ig-like C2-type 1.

Ig-like C2-type 2.

Ig-like C2-type 3.

ITM morif.

By similarity.

By similarity.

By similarity.

By similarity.

By similarity.

N-linked (GlCNAc. ...) (Potential).

N-linked (GlCNAc. ...) (Potential).

N-linked (GlCNAc. ...) (Potential).

N-linked (GlCNAc. ...) (Potential).

N-linked (GlCNAc. ...) (Potential).

N-linked (GlCNAc. ...) (Potential).

N-linked (GlCNAc. ...) (Potential).
                                                                                                                           Sialic acid binding Ig-like lectin
Extracellular (Potential).
Potential.
Cytoplasmic (Potential).
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PROSITE; PS50835; IG LIKE; 3.
PROSITE; PS00290; IG_MHC; 1.
Alternative splicing; Cell adhesion; Glycoprotein;
Immunoglobulin domain; Lectin; Phosphorylation; Repeat; Signal;
Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 2173; DB 1; Length 6; Pred. No. 6.2e-129; 50; Mismatches 111; Indels
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E -> A (in Ref. 2).
A -> G (in Ref. 2).
FD0EA1936156E5A8 CRC64;
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353
74544 MW;
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63.3%;
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686 AA;
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CONFLICT
SEQUENCE
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CARBOHYD
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182 DAVSFQESRPHTSNYSVLSFIPGLQHHDTELTCQLDFSR--MSTQRTVRLRVAYAPRSLA 239
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                                                                                                                                                                                                           GNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGE 364
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                                                                                                                                                                                                                                                                                                                                      418 FICAAQNPLGAQRISLSLSVHYPPQMSSPSCSWEAKGLHCNCSSRAWPAPSLRWRLGEGL 477
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STRAIN-C57BL/6J; TISSUE-Thymus;
STRAIN-C57BL/6J; TISSUE-Thymus;
The FANTOM Consortium,
the RIARTOM Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
                                                              240 ISIFHDNVSV--PDLHENPSHLEVQQQQSLRLLCTADSQPPATLSWVLEDQVLSWSSPVG
                                                                                                                                              SRTLALELEWVKAGDSGHYTCQAENRLGSQQHTLDLSVLYPPQDLRVTVSQANRTVLEIL
                                                                                                                        245 PRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLENL
                                                                                                                                                                                                                                      RNAISLPVLEGQSLCLVCVTYSNPPANVSWAWVTQTLIPIQSSEPGVLELPLVQREHEGE
                                                                                                                                                                                                                                                                                                                                                                                                         185 ISISRDNTPALEPOPOGNVPYLEAQKGOFLRLLCAADSOPPATLSWVLQNRVLSSSHPWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                485 LISTAFSNGAFLGIGITALLFLCLALIMKILPKRRIQTETPRPRFSRHSTILDYINVVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus 3 days neonate thymus CDNA, RIKEN full-length enriched library, clone:A630096C01 product:weakly similar to SIALIC ACID-BINDING LECTIN (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QEELHYATLNFPGVRPRPEARMPKGTQADYAEVK 637
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"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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MEDLINE=99279253; PubMed=10349636;
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STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=21085660; PubMed=11217851;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular analysis of human Siglec-8 orthologs relevant to mouse eosinophils: identification of mouse orthologs of Siglec-5 (mSiglec-F) and Siglec-10 (mSiglec-G)."; Genomics 82:521-530(2003).
                                                                                                                                                                                                                                                                                                  LLGPSCSWEAEGLHCSCSSQASPAPSLRWWLGEELLEGNSSQDS7EVTPSSAGPWANSSL
                                                                                                                                          ------KKGLISTAFSNGAFLGIGITALLFLCLA
                                                                                                                                                                                  510 LIIMKILPKRRTQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPG
                                                                                                                                                                                                                    296 LIIMKILPKRRIQTBTPRPRFSRHSTILDYINVVPTAGPLVQKRNQKATPSSPRTPLPPG
                                                                                                                                                                                                                                                                     570 APSPESKKNOKKOYOLPSFPBPKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGT
                                                                                                  450 SLHGGLSSGLRLRCEAWNVHGAQSGSILQLPDKKGLISTAFSNGAFLGIGITALLFLCLA
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MEDLINE=22921108; PubMed=14559209;
Aizawa H., Zimmermann N., Carrigan P.E., Lee J.J., Rothenberg M.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:2443630; Siglec10.
InterPro: IPR007110; Ig-11ke.
Fram: PF00047; Ig:2.
SMART; SM00408; IG-2.
SMART; SM00408; IG-2.
SMART; SM00408; IG-11ke.
SEQUENCE 688 As; 76884 MM; 21A619E1500BFA76 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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Best Local Similarity 54.9
Matches 381; Conservative
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Name=Siglec10;
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                                                       268
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298 SRTLALELPWVKAGDSGHYTCQAENRLGSQQHTLDLSVLYPPQDLRVTVSQANRTVLEIL
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ISIFHDNVSV--PDLHENPSHLEVQQQQSLRLLCTADSQPPATLSWVLEDQVLSWSSPVG
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28-FEB-2003 (Rel. 41, Last sequence update)
01-OCT--2004 (Rel. 45, Last annotation update)
Sialic acid binding Ig-like lectin 5 precursor (Siglec-5) (Obesity-binding protein 2) (OB binding protein 2) (OB binding protein-2) (OB-BP2) (CD33 antigen-like
                                                                                                                                                                                                                                                                                                                                                                                TISSUBEERTCHOOLEUkemia;
MEDLINE=99357812; PubMed=10428856;
MEDLINE=99357812; PubMed=10428856;
Balea N. Brinkman-Van der Linden E.C.M., Altmann S.W., Gish K.C.,
Balsaubramanian S., Timans J.C., Peterson D., Bell M.P., Bazan J.F.
Varki A., Kastelein R.A.;
Varki A., Kastelein R.A.;
immunoglobulin superfamily.";
J. Biol. Chem. 274:22729-22738(1999).
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D., Bell M.P., Bazan J.F.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae, Homo
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MEDLINE=9840280; PubMed=9731071;
Cornish A.L., Freeman S., Forbes G., Ni J., Zhang M., Cepeda M., Gentz R., Augustus M., Carter K.C., Crocker P.R.;
Gentz R., Augustus M., Carter K.C., Crocker P.R.;
"Characterization of siglec-5, a novel glycoprotein expressed on myeloid cells related to CD33.";
Blood 92:2123-2132(1998).
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Balasubramanian S., Timans J.C., Peterson
Varki A., Kastelein R.A.,
J. Biol. Chem. 274:28058-28058(1999).
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Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

GARAIN=C57BL/6J; TISSUB=Thymus;
Adachi U., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
A Fukuda S., Furuno M., Hanagaki T., Hara A., Hashitume W.,
A Hayashida K., Hayateu N., Hiramoto K., Hiraoka T., Hirozane T.,
A Hayashida K., Ishii Y., Itoh M., Kagawa T., Kasukawa T.,
A Katoh H., Kawai J., Kojima Y., Kondo M., Kouda M., Koya S.,
A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
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R EMBL; AK042488; BAC31272.1;
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                               STRAIN=C57BL/6J; TISSUE=Thymus; MEDILINE=20499374; PubMed=11042159; Carminci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630 (2000).
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Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Akiyama J., Nishi K., Hatsumai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watshiwagi K., Foneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rikik integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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Pred. No. 4.4e-97;
8; Mismatches 148; Indels
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GO; MGI:2443630; Siglec10.

GO; GO:0005529; F:sugar binding; IEA.

GO; GO:000157; P:heterophilic cell adhesion; IEA.

InterPro; IPR003110; Ig-like.

InterPro; IPR003598; Ig_C2.
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- -!- FUNCTION: Putative adhesion molecule that mediates sialic-acid dependent binding to cells. Binds equally to alpha2,3-linked and alpha2,6-linked sialic acid. The sialic acid recognition site may be masked by cis interactions with sialic acids on the same cell surface.
- -!- SUBCELULIAR LOCATION: Type I membrane protein.
 -!- SUBCELULIAR LOCATION: Type I membrane protein.
 -!- TISSUE SPECIFICITY: Expressed by monocytic/myeloid lineage cells. Found at high levels in professed blood leukocytes, spleen, bone marrow and at lower levels in lymph node, lung, appendix, placenta, pancreas and thymus. Expressed by monocytes and neutrophils but absent from leukemic cell lines representing early stages of myelomonocytic differenciation.
 -!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in modulation of cellular responses. The phosphorylated ITIM motif can bind the SH2 domain of several SH2-

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMB contestation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). containing phosphatases.
--- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC (stallic acid binding 1g-like lectin) family.
--- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
--- SIMILARITY: Contains 1 immunoglobulin-like V-type domains.

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PROSITE; PS50855, 1G LIKE; 3.
PROSITE; PS50859; IG_MHC; 1.
Antigen; Cell adhesion; Glycoprotein; Immunoglobulin domain; Lectin; Polymorphism; Repeat; Signal; Transmembrane.
POLYMORPHISM: Repeat; Signal; Potential.
CHAIN
17 551 Sialic acid binding Ig-like lectin 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Potential.
Stalic acid binding Ig-like lectin 5.
Extracellular (Potential).
Cytoplasmic (Potential).
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Ig-like C2-type 1.
Ig-like C2-type 2.
ITIM motif.
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EMBL; U71383; AAB70703.1; -.
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InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
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HSSP; Q9Y286; 107S.
Genew; HGNC:10874; SIGLEC5.
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RESULT 9

SLAM-LIKE MOTIF. By similarity.

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SULFID 41 101 By similarity. SULFID 164 213 By similarity. SULFID 269 213 By similarity. REGHYD 100 104 N-linked (GlcNAc) (Potential). REGHYD 231 210 N-linked (GlcNAc) (Potential). REGHYD 253 253 N-linked (GlcNAc) (Potential). REGHYD 378 378 N-linked (GlcNAc) (Potential). REGHYD 394 384 N-linked (GlcNAc) (Potential). REGHYD 393 394 N-linked (GlcNAc) (Potential). REGHYD 393 N-linked (GlcNAc) (Potential). REGHYD 393 N-linked (GlcNAc) (Potential). RIANT 72 72 74TId=VR. ATIG=VAR 014249 77 77 FTIG=VAR 014249 77 77 RIANT 322 72 74TId=VAR 014249 RIANT 322 322 75 77 RELICT 358	Match 11.0%; Score 1047; DB 1; Length 551; Local Similarity 39.4%; Pred. No. 6.6e-58; es 256; Conservative 76; Mismatches 203; Indels 114; Gaps	2 ILPLLLSSLL-GGSQAMDGRFWIRVQESVWVPBGLCISVPCSFSYPRQDWTGSTPAYQYW	61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV	21 BRGSYVRYNFWNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP	21 BRGRDVKYSYQQNKLNLEVTAL	181 RDLVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRV 181 RDLVISISRDNTPALEPQPQGNVPYLEAQKRV 181 RDLVISISRDTHFLEPLESGRPTRLSCSLPGSCEAGPPLTFSWTGNA 183IEXPDIHFLEPLESGRPTRLSCSLPGSCEAGPPLTFSWTGNA 183	37 LSSSHPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQORALDLSVOYPPENLKVWV	85 I.SPLDPRTTRSSELTLTPRPEDHGTNLTCQMK-ROGAQVTTERTVOLAVSYAPOTITIF- 94 SQANRTVLENIGNGTSLPVLEGGSLCLVCVTHSSPPARLSWTORGQVLSPSOPSDPGVLE	VLECCALKLILCERFSNEFARISM: CGSFALLNFFFSNEGTED PLGSQHVSLSLSVHYSPKTLGPSCSWEABGLHCSCSSQASPA	:	14 PSLEWWIGEELLEGNSSODSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAOS	1 PSLCWRLEEKPLEGNSSQGSFKVNSSSAGPWANSSLILHGGLSSDLKVSCKAWNIYGSQS	474 GSILOLPDKKGLISTAFSNGAFIGIGITALIFICALIIMKILPKRRIQTETPRPRFSRH	PRIPL-PPGAPSPESKKNOKKOYQLPSFPEPK	479 BDPIMGIITSGSRKKPWPDSPGDQASPPGDAPP	3 SSTQAPESQESGELHYATLNFFGVRPRPEARWPKGTQADYAEVK 63	ELHYASISFSEMKSREPKDQEAPSTTEYSE
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InterPro; IPR003598; Ig_c2.
Pfam; PF00047; ig; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       354 LPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPA 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MLPLLLLLPLLWGGSLQEKPVYELQVQKSVTVQEGLCVLVPCSFSYPWRSWYSSPPLYVYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                   homo sapians (Human).
Eukaryota: Metazoma: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76; Mismatches 204; Indels 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           551 AA; 60688 MW; 6EEA2B6B29B59304 CRC64;
                                                 02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Sialic acid binding Ig-like lectin 5.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1039; DB 2;
Pred. No. 2.1e-57;
                      551 AA
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                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
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                      AAH29896
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.ch).
                                                                                                                                                                                                                                                                          478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or clusters.";

Biol. Chem. 276:45128-45136 (2001).

Provident binding to cells. Preferentially binds to alpha2.3-
linked stalic acid. The stalic acid recognition site may be masked by cis interactions with stalic acids on the same cell surface.

SUBCELULLAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: Predominantly expressed by immature monocytic/myeloid lineage cells in bone marrow. Also found at lower levels in mature neutrophils and monocytes.

DOMAIN: Contains I copy of a cytoplasmic motif that is referred to as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This
                                                                                                                                                                                                                                                 474 GSILQLPDKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRH
PSLRWWLGEELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQS
                                                                                             PSLCWRLEEKPLEGNSSQGSFKVNSSSAGPWANSSLILHGGLSSDLKVSCKAWNIYGSQS
                                                                                                                                                                                                                                                                                                                                                                            534 STILDYINVVPTAGPLAQKRNQKATPNSPRTPL-PPGAPSPESKKNQKKQYQLPSFPEPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21576254; PubMed=11579105; DOI=10.1074/jbc.M108573200; Angata T., Hingorant R., Varki N.M., Varki N. S., "Cloning and characterization of a novel mouse Siglec, mSiglec-F: differential evolution of the mouse and human (CD33) Siglec-3-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               motif is involved in modulation of cellular responses. The phosphorylated ITIM motif can bind the SH2 domain of several SH2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   containing phosphatases.
SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC (stails catch binding 1g-like lectin) family.
SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              593 SSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQA----DYAEVK 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0920G3;
28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 44, Last sequence update)
01-0CT-2004 (Rel. 45, Last annotation update)
Sialic acid binding Ig-like lectin-F precursor (mSiglec-F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         479 ED-----PIMGTITSGSRKKPWPDSAGDQASPPGDAPP
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497 SNIALGYPIQGHLNEPGSQTQKEQPPLATVPDTQKDEPELHYASLSFQGPMP-PKPQNTE 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 REGANIFSGSPVATNDPORSVLKEAQGRFYLMGKENSHNCSLDIRDAOKIDTGTYFFRLD 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 KAVTETTKGAPVATNHQSREVEMSTRGRPQLTGDPAKGNCSLVIRDAQMQDESQYFFRVE 1.21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    407 SSQASPAPSLRWWLGEELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAW 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular analysis of human Siglec-8 orthologs relevant to mouse essinophils: identification of mouse orthologs of Siglec-5 (mSiglec-F) and Siglec-10 (mSiglec-G)."; Genomics 82:521-530(2003).
EXBL: AY21.0401; AA048274.1; -. HSSP; Q9Y286; 107S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 DIVISISRDNTPALEPQPQGNVPYLEAQKGOFLRLIC----AADSQPPATLSWV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 STLVS------GNSTKLLCSVPWACEQGTPPIFSWMSSALTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230 QKMTIRVSWGDDTGTKVLQSGASLQIQEGESLSLVCMADSNPPAVLSWERPTQ--KPFQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 LLPLLWA----GCLATDG-YSLSVTGSVTVQBGLCVFVACQVQYP----NSKGPVFGYWF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 LGHRITLSSELNLTPRP------QDNGTNLTCQV-NLPGTGVTVERTQQLSVIYAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=BALB/C;
Display=22921108; PubMed=14559209;
Aizawa H., Zimmermann N., Carrigan P.E., Lee J.J., Rothenberg M.E.
Bochner B.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
Pfam; PF00047; ig; 2.
SWART; SM0408; IG-2.
SPROSITE; PS0935; IG LIKE; 2.
SEQUENCE 523 AA; 56326 MW; 85342501E33817EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                  Q80ZE2;
01-JUN-2003 (TYEMBLrel. 24, Cr
01-JUN-2003 (TYEMBLrel. 24, La
01-MAR-2004 (TYEMBLrel. 26, La
Siglec-F variant.
Name-Siglec5;
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Best Local Similarity 38.59
Matches 209; Conservative
                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                       628 GTQADYAEVK 637
                                                                                                                                                                             556 AMKSVYTĖIK 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 -GS-VKYSFQKS--MLSVLVIALTEVP---NIQVT------144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 KAVTETTKGAPVATNHQSREVEMSTRGRPQLTGDPAKGNCSLVIRDAQMQDESQYFRVE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 REGANIFSGSPVATNDPORSVLKEAQGRFYLMGKENSHNCSLDIRDAQKIDTGTYFFRLD 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 RGSYVRYNFMNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLC----AADSQPPATLSWV----- 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----GNSTKLLCSVPWACEQGTPPIFSWMSSALTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232 LQNR-VLSSSHPWGPRPLGLELPGVKAGDSG-RYTCRAENRLG---SQQRALDLSVQYPP 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 LGHRITLSSELNLTPRP------QDNGTNLTCQV-NLPGTGVTVERTQQLSVIYAP 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      287 ENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQP 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230 OKMTIRVSWGDDTGTKVLQSGASLQIQEĞESLSLVCMADSNPPAVLSWERPTQ--KPFQL 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYSPKLLGPSCSWEAEGLHCSC 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   288 STPAELQLEPRAELEDQGKYICQAQNSQGAQTASVSLSIRSLLQLLGPSCSFEGQGLHCSC 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSQASPAPSLRWWLGEELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAW 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     467 NVHGAQSGSILQLPDKKGLISTAFSN-----GAFLGIGITALLFLCLALII--MKIL 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDNRVQRATILLVSGPK--VSQAGKSETSRGTVLGAIWGAGLMALLAVCLCLIFFTVKVL 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 LLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 LLPLLWA----GCLATDG-YSLSVTGSVTVQEGLCVFVACQVQYP----NSKGPVFGYWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                          Potential.
Sialic acid binding Ig-like lectin-F.
Extracellular (Potential).
Potential.
Cycoplasmic (Potential).
Ig-like V-type.
Ig-like C2-type 1.
ITM morif.
SLAM-LIXE MOTIF.
                                                           SMART; SM00408; IGC2; 1.

PROSITE; PS50835; IG LIKE; 2.

Cell adhesion; Glycoprotein; Immunoglobulin domain; Lectin; Repeat;
Signal; Transmembrane.

Signal; Transmembrane.

FORMIN 17 569 Sialic acid binding Ig-like lectin-F.

TRANSTEM 440 660 Potential.

CHAIN 419 Potential.

CHAIN 460 Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 24.8%; Score 837; DB 1; Length 569; Best Local Similarity 35.7%; Pred. No. 1.3e-44; Matches 239; Conservative 80; Mismatches 207; Indels 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Potential)
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N-linked (GlcNAc. . .)
N-linked (GlcNAc. . .)
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569 AA;
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                                                                                             SDNRVQRATILLVSGPK--VSQAGKSETSRGTVLGAIWGAGLMALLAVCLCLIFFTVKVL 465
NVHGAQSGSILQLPDKKGLISTAFSN-----GAFLGIGITALLFLCLALII--MKIL 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isoid=Q9NYZ4-3; Sequence=VSP_002560;
TISSUE SPECIFICITY: Expressed specifically on eosinophils.
DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to
as the immunoreceptor tyrosine-based inhibitor motif (TIIM). This
motif is involved in modulation of cellular responses. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytoplasmic tyrosine-based motifs, and mapping of the siglec8 gene."; Biochem. Biophys. Res. Commun. 278:775-781(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Eosinophil;
MEDLYRE=2092847; PubMed=10625619;
Floyd H., Ni J., Cornish A.L., Zeng Z., Liu D., Carter K.C., Steel J Crocker P.R.;
Crocker P.R.;
"Siglec-8. A novel eosinophil-specific member of the immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 3).

MEDLINE-2014554, PubMed=10856141,

Kikly K.X., Bochner B.S., Freeman S.D., Tan K.B., Gallagher K.T.,

D'Alessio K.J., Holmes S.D., Abrahamson J.A., Erickson-Miller C.L.,

Muddock P.R., Tachimoto H., Schleimer R.P., White J.R.;

"Identification of SAF-2, a novel siglec expressed on eosinophils,
mast_cells, and basophils.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 2).

SLOYd H., Zhang J.O., Crocker P.R.;

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

-I FUNCTION: Putative adhesion molecule that mediates sialic-acid dependent binding to cells. Preferentially binds to adhas, 3-

Innked sialic acid. Also binds to alpha2,6-linked sialic acid.

sialic acid recognition site may be masked by cis interactions with sialic acids on the same cell surface.

-I SUBCELDULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=20549027, PubMed=11095983; DOI=10.1006/bbrc.2000.3866;
Foussias G., Yousef G.M., Diamandis E.P.;
"Molecular characterization of a siglec8 variant containing
                                                                                                                                                                                                                                                                                                                                                                                                                                       (Siglec-8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
01-077-2004 (Rel. 45, Last annotation update)
sialic acid binding Ig-like lectin 8 precursor
(Sialoadhesin family member-2) (SAF-2).
Name-SIGLEC8; Synonyms-SAF2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Allergy Clin. Immunol. 105:1093-1100(2000).
                                                                                                                                                                                                                                                                                                                       499 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=1; Synonyms=Long;
IsoId=Q9NYZ4-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Chem. 275:861-866(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 3).
                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                             PKR 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                         RKK 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=2;
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                                                                                                                408
                                                                                                                                                             517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTSTVRLDVSY -> D (in isoform 2).
/FTId=VSP 002559.
GPLTESWKDGNPLKKPPPAVAPSSGEEGELHYATLSFHKVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PQDPQGQEATDSEYSEIKIHKRETAETQACLRNHNPSSKEV
RG -> VSDVGFSTPSIQPGHL (in isoform 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTHRPDILILGTLESGHSRNLTCSVPWACKQGTPPMISWI
GASVSSPGPTTARSSVLTLTPKPQDHGTSLTCQVTLPGTGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MLLLLLLLLLTLLTKGTKGMEGDRQYGDGYLLQVQELVTVQEGLCVHVPCSFSYPQDGWTDSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MLLPLLLSSLLGGSQAMDG-----RFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
several SH2-
                  SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC (stails caid binding Ig-like lectin) family. SIGLEC SIMILARITY: Contains 2 immunoglobulin-like C2-type domains. SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sialic acid binding Ig-like lectin 8.
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.4%; Score 721.5; DB 1; Length 499; 30.8%; Pred. No. 2.1e-37; ive 80; Mismatches 152; Indels 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Potential)
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                                                                                                                                                                                                                                                                                                                       EMBL; AF287892; AAG00573.1; -.
EMBL; AF287892; AAF34702.1; -.
EMBL; AF195092; AAF27622.1; -.
EMBL; AF395024; AAK55140.1; -.
EMBL; AF310234; AAK55140.1; -.
HSSP; Q9Y286; 1078.
Genew; HGNC:10877; SIGLEC8.
MIM, 605839; -.
GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0016529; F:sugar binding; TAS.
GO; GO:0004888; F:transmembrane receptor activity; TAS.
GO; GO:0001165; P:signal transduction; TAS.
InterPro; IPR003598; Ig-1ike.
  phosphorylated ITIM motif can bind the SH2 domain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  086EFF989B74123C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potential.
Cytoplasmic (Potential).
Ig-like V-type.
Ig-like C2-type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIAM-LIKE MOTIF.

By similarity.
By similarity.
By similarity.
By similarity.
N-linked (GloNAc...) (()
N-linked (GloNAc...) (()
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/FTId=VSP 002560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 30.8 Matches 207; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      499 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; ig;
SMART; SM00408; IG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   416
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DOMAIN
TRANSMEM
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SITE
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DISULFID
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VARSPLIC
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293 LSWTRGSLTLCPSRSSNPGLLELPRVHVRDEGEFTCRAQNAQGSQHISLSLS---- 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PVHGYWFRAGDRPYQDAPVATNNPDRBVQABTQGRFQLLGDIWSNDCSLSIRDARKRDKG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     452 HGGLSSGLRLRCEAWNVHGAQSGSILQLPDKKGLISTAFSNGAFLGIGITALLFL--CLA 509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 PAYGYWFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDES 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212 QFLRILCAADSQPPATISWVLQNRVLSSSHPWGPRPLGLELPGVKAGDSGRYTCRAENRL 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYSPKLL 3:91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          392 GPSCSWEAEGIHCSCSSOASPAPSLRWWIGEELLEGNSSODSFEVTPSSAGPWANSSLSL 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         381 FILV----RSCRKKSARPAAGVGDTGMEDAKAIRGSASQGPLTESWKD----GNPLKKP 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPGAPSPESKKNOKKOYOLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPR-PEARM 625
Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----APSSGE-EGELHYATLSFHKVKPQDPQGQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MLLPLLLSSLLGGSQAMDG-----RFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MILILILILPILLWGTKGMEGDRQYGDGYLLQVQELVTVQEGLCVHVPCSFSYPQDGWTDSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 QYFFRVERGSYVRYNFMNDGFF----LKVTVLSFTPRP-----QDHNTDLTCHVDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 SRK------GVSAQRTVRLRVAYAPRDLVISISRDNTPALEPQPQGNVPYLEAQKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  510 LIIMKILPKRRIQTETPRPRFSRHSTILDYINVV---PTAGPLAQKRNQKATPNSPRTPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----VTLPG--TGVTTTSTVR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        272 GSQQRALDISVQYPPENIRVMVSQANRTVLENIGNGTSLPVLEGQSLCLVCVTHSSPPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 -----LDVSYPPWNLTMTVFQGDATASTALGNGSSLSVLEGQSLRLVCAVNSNPPAR
                                                                                                                                                                                                                                                                                                                                                                                           Length 499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GTSRPVSQVTLAAVG-
                                                                                                                                                                                                                                                                                                                                                                                           21.3%; Score 718.5; DB 2; Length 30.8%; Pred. No. 3.3e-37; ive 79; Mismatches 153; Indels
                                                                                                                                      Strausberg R.; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases. EMBL BC05319; AAH53191; -. InterPro; IRR07110; Ig-1ike. InterPro; IPR003598; Ig-2. Pfam; PF00047; ig: 2.
                                                                                                                                                                                                                                                                                                                                                    54052 MW; CA32FEF7A88A7D3D CRC64;
                      and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                             SMART; SM00408; IGG2; 1.
PROSITE; PS50835; IG LIKE; 2.
Hypothetical protein.
SEQUENCE 499 AA; 54052 MW;
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 30.89
Matches 207; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              464 -EATDSEYSEIK 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346 ----QNEGT---
                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      432 PPAV----
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SILL HUMAN
ID SILL HUMAN
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RIAUsner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RIAUsner R.D., Collins B., Butcow K.H., Schaefer C.F., Bhat N.K.,
A lischen, S.F., Zeeberg B., Butcow K.H., Schaefer C.F., Bhat N.K.,
Diatchenco, L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Changtcheron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.G., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rahessley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Markeyley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Markeyley M.J., Markeyley R.W., Butterfield Y.S.,
Markeyley M.J., Narkeyley R.W., Butterfield Y.S.,
Markeyley M.J., Markeyley U., Smailus D.B., Schnerch A., Schein J.B.,
    121 SYFFRLERGS-MKWSYKSQLNYXTKQLSVFVTALTHRPDILILGTLESGHSRNLTCSVFW 179
                                                                         162 SRK------GVSAQRTVRLRVAYAPRDLVISISRDNTPALBPQPQGNVPYLBAQKG 211
                                                                                                                                                                   212 QFLRLLCAADSQPPATLSWVLQNRVLSSSHPWGPRPLGLELPGVKAGDSGRYTCRAENRL 271
                                                                                                                                                                                                                                                              272 GSQQRALDLSVQYPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPAR 331
                                                                                                                                                                                                                                                                                                        241 -----LDVSYPPWNLTMTVPQGDATASTALGNGSSLSVLEGQSLRLVCAVNSNPPAR 292
                                                                                                                                                                                                                                                                                                                                                    332 LSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYSPKLL 391
                                                                                                                                                                                                                                                                                                                                                                                                  293 LSWTRGSLTLCPSRSSNPGLLELPRVHVRDEGEFTCRAQNAQGSQHISLSL----- 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                              392 GPSCSWEAEGLHCSCSSQASPAPSLRWWLGEELLEGNSSQDSFEVTPSSAGPWANSSLSL 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----APSSGE-EGELHYATLSFHKVKPODPQGQ- 463
                                                                                                                                                                                                                -----VTLPG--TGVTTTSTVR-----
                                                                                                                       180 ACKQGTPPMISWIGASVS-----SPGP---TTARSSVLTLTPKPQDHGTSLTCO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----GTSRPVSQVTLAAVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
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464 -EATDSEYSEIK 474
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Tones S.J., Marra M.A.;
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NCBI_TaxID=9606;
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AC 905PO1: 091PO1: 401PO1 (1911)

20 FORD-1003 (Rel. 41, Dec. 401 Engence update)

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      Isoid=096PQ1-1; Sequence=Displayed;
Name=Short; Synonyms=SLG-S;
Isoid=096PQ1-2; Sequence=VSP 002566;
Isoid=096PQ1-2; Sequence=VSP 002566;
Isoid=096PQ1-2; Sequence=VSP 002566;
In SPECIFICITY: The short Isoform is highly expressed in spleen, small intestine and adrenal gland; it is lower expressed in thyroid, placenta, brain, stomach, bone marow, spinal chord and beast. The long isoform is highly expressed in spleen, small intestine marrow; it is lower expressed in thyroid, placenta, thymus, trachea, stomach, lung, adrenal gland, fetal brain and teetis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LILLIPPLLCGRVGAKEQKDYLLTMQKSVTVQBGLCVSVLC
SRSYPDQMATASDPVHAYWRPAQBHVSRNIPPATNNRARAV
QESTREFHLLGPDQNKDCTLSIRDTRESDAGTYFCVERG
NMKWNYKYDQLSVNV -> PLLWANBERDSGGWADPRFS
                                                                                                                                                                    DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to
as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This
motif is involved in modulation of cellular responses. The
phosphorylated ITIM motif can bind the SH2 domain of several SH2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sialic acid binding Ig-like lectin-like
                                                                                                                                                                                                                                  containing phosphatases.
SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC (siallic acid binding Ig-like lectin) family.
SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
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(Potential).
(Potential).
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(Potential).
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Cytoplasmic (Potential)
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Ig-like V-type 1.
Ig-like C2-type 1.
Ig-like C2-type 2.
ITIM motif C2-type 2.
ITIM motif Shan-like MOTIF.
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EMBL; AF277806; AAK51234.1; --
EMBL; AF282256, AAK71521.1; --
EMBL; AX380140; AAR380307.1; --
EMBL; BC035809; AAH35809.2; --
HSSP; QSY286; 1078.
Genew; HGNC:15482; SIGLECLI.
MIM; 606094; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interPro, IPR007110; Ig-like.
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127 RYNEWNDGFFLKVTVLSFTPR-----PQDHNTDLTCHVDFS-RKGVSAQRTVRLRVAY 178
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SIGNAL 1 20
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Matches 198; Conserva
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                                                                                                                                                                                                    RYNFMNDGFFLKVTVLSFTPR-----PQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYA 179
                                                                                                                                                                                                                                                                        256 KWNYIYDKLSVHVTALTHMPTFSIPGTLESGHPRNLTCSVPWACEQGTPPTITWMGASVS 315
                                                                                                                                                                                                                                                                                                                                                         240 SHPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRT 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       478 QLPDKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTIL 537
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                                                                                                                              7 LSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWFKAVTE 66
                                                                                                                                                379 ASTTLRNGSALSVLEGQSLHLVCAVDSNPPARLSWTWGSLTLSPSQSSNLGVLELPRVHV
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BEDLINE-15123976, PubMed=11546777, DOI=10.1074/jbc.M105926200,
Angata T., Varki N.M., Varki A.;
"A second uniquely human mutation affecting sialic acid biology.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pan troglodytės (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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0951H0;
28-FFBB-2003 (Rel. 41, Created)
28-FFBB-2003 (Rel. 45, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
shaltc acid binding Ig-like lectin-like 1 precursor (Siglec-like Name=SIGLBCL1;
                                                                                    Pred. No. 5.7e-36;
72; Mismatches 176; Indels 179;
                                                                      Length 595;
P -> T (in dbSNP:2034891).
/FTId=VAR_014259.
               FTId=VAR 014259.
-> W (in Ref. 3).
D05662176274C5C3 CRC64;
                                                                        DB 1;
                                                                   Score 700.5; DB 1
Pred. No. 5.7e-36;
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                                             64984 MW;
                                                                      Query Match
Best Local Similarity 31.5%;
Matches 196; Conservative 7
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595 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                -1. SUBCELLULAR LOCATION: Type I membrane protein.
-1. DOMAIN: Contains I copy of a cytoplasmic motif that is referred to as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in modulation of cellular responses. The phosphorylated frum motif can bind the SH2 domain of several SH2-containing phosphases to the immunoglobulin superfamily. SIGLEC (stail can bind the SH2) family. SIGLEC (stail can bind in graph family graph family graph family graph family graph family family. SIGLEC (stail binding 1g-like lectin) family.
-1. SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Potential.
Sialic acid binding Ig-like lectin-like
     Mod. Chem. 276:40282-40287(2001).
FUNCTION: Putantive adhesion molecule that mediates sialic-acid dependent binding to cells. The sialic acid recognition site may be masked by cis interactions with sialic acids on the same cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR07110; Ig-like.
InterPro; IPR03598; Ig_c2.
Pfan; PF00047; Ig; 4.
SWART; SM00408; IG_c2; 1.
PROSITE; PS50835; IG_LIKE; 3.
Cell adhesion; Glycoprotein; Immunoglobulin domain; Lectin; Repeat;
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(ytoplasmic (Potential).

(ytoplasmic (Potential).

Ig-like V-type 1.

Ig-like (2-type 1.

Ig-like (2-type 2.

ITIM motif.
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N-linked (GlCNAC.).
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276:40282-40287(2001)
Chem.
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Dp	258	KWNYIYDKLSVHVTALTHLPTFSIPGTLESGHPRNLTCSVPWAÇEQGTPPTITWMGA 314
ò	179	APRDLVISISRDNTPALEPOPOGNVPYLEAQKGOFLRLLCAADSOPPATLSWVLONRVLS 238
QQ	315	SVSSLEPTISRSSMLSLIPKPQDHGTSLTCQ->345
ò	239	SSHPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPBNLRVWVSQANR 298
Db	346	. THE STATE OF THE
ò	299	TVLENIGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQ 358
QQ	380	TASTTLRNGSALSVLEGQSLHLVCAVDSNPPARLSWTWGSLTLSPSQSSNLGVLELPRVH 439
ò	359	VEHEGEFICHARHPLGSQHVSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPAPSL 416
QQ	440	VKDEGEFTCRAQNPLGSQHISLSLSLQNEYTGKMRPI 476
ò	417	RWWLGEELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGSI 476
qq	477	:
δý	477	LOLPDKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTI 536
qq	482	
ò	537	LDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKS 593
QQ	523	
ογ	594	PGVRPRPEARMPKGTQA
qq	562	

Search completed: November 5, 2004, 13:57:42 Job time : 143.458 secs

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1 MLPFLLSSLLGGSQAMDGR.....RPEARMPKGTQADYAEVKFQ 639
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Sequence 3
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US-09-046-736-2
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Maximum Match 100%
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                                             - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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28 200.5 5.9 734 2 US-08-389-459A-17 Sequence 17, Appl 30 200.5 5.9 734 3 US-08-997-867A-17 Sequence 17, Appl 30 200.5 5.9 1953 4 US-08-997-867A-17 Sequence 17, Appl 31 199.5 5.9 1953 4 US-09-917-254-92 Sequence 4599, Appl 32 197.5 5.8 280 4 US-09-917-254-92 Sequence 92, Appl 33 197.5 5.8 180 4 US-09-130-158A-2 Sequence 2, Appl 34 193.5 5.7 1209 4 US-09-130-158A-2 Sequence 2, Appl 34 193.5 5.7 1209 4 US-09-130-158A-2 Sequence 2, Appl 37 191.5 5.7 424 6 5169835 Sequence 1, Appl 37 191 5.7 529 3 US-09-389-586-31 Sequence 31, Appl 39 188.5 5.6 630 3 US-09-991-326-14 Sequence 14, Appl 40 188.5 5.6 630 3 US-09-991-326-14 Sequence 14, Appl 41 188.5 5.6 612 3 US-09-991-326-14 Sequence 17, Appl 44 187.5 5.6 612 3 US-09-991-326-11 Sequence 11, Appl 45 187.5 5.6 612 3 US-09-991-326-11 Sequence 11, Appl	ALIGNMENTS	RESULT 1 US-08-896-537A-2 Sequence 2, Application US/08896537A Patent No. 6590088 GENERAL INFORMATION: APPLICANT: APPLICANT: Ni, Jian APPLICANT: Rosen, Craig A. TITLE OF INVENTION: CD33-Like Protein FILE REFERENCE: 1489 04800L); FILE REPERENCE: 1489 04800L); CURRENT APPLICATION NUMBER: US/08/896,537A CURRENT FILING DATE: 1996-07-19 NUMBER OF SEQ ID NOS: 12 SOFTWARE: Patentin version 3.1 SEQ ID NO 2 LENGTH: 551 TYPE: RRT TYPE: RRT TYPE: RRT TYPE: RRT TYPE: RRT TYPE: RRT TYPE: RRT TYPE: RRT TYPE: RRT TYPE: RRT TYPE: RRT TYPE: RRT TYPE: RRT TYPE: RRT	Query Match 30.6%; Score 1033; DB 4; Length 551; Best Local Similarity 39.0%; Pred. No. 4.7e-80; Matches 253; Conservative 78; Mismatches 204; Indels 114; Gaps 15;	QY 2 LLPLLISSLL-GGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW 60 :	QY 61 FKAVTETTKGAPVATNHQSREVEMSTRGRFOLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120	QY 121 ERGSYVRYNFWNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAXAP 180	QY 181 RDLVISISRDNTPALEPQPQGNVPYLEAQKGQFLKLLCAADSQPPATLSWVLQNRV 236 :
8 8 0 0 1 1 2 K 4 4 0 0 1 1 2 K 4 4 0 0 1 1 2 K 4 5 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		MINDIN MI	Query Ma Best Loc Matches	ර් සි	o S		

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243 --RNGIALEILQNTSYLPVLEGQALRILCDAPSNPPAHLSWFGGSPALNATPISNTGILE 300

LSSSHPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQ----QRALDLSVQYPPENLRVMV

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                      301 LRRVRSAEKGGFTCRAQHPLGFLQIFLNLSVYSLPQLLGPSCSWEAEGLHCRCSFRAWPA 360
                                                                                                                          361 PSLCWRLEEKPLEGNSSQGSFKVNSSSPGPWANSSLILHGGLNSDLKVSCKAWNIYGSQS 420
                                                                                                                                                                     474 GSILQLPDKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRH 533
                                                                                                                                                                                              414 PSLRWWLGEELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQS 473
                                                                                                                                                                                                                                                       534 STILDYINVVPTAGPLAQKRNQKATPNSPRTPL-PPGAPSPESKKNQKKQYQLPSFPEPK 592
354 LPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                # Perent No. 022373.
# GENERAL INFORMATION:
# PELICANT: Althann, Scott W.
# APPLICANT: Rock, Fernando L.
# APPLICANT: Bazan, J. Fernando
# APPLICANT: Mastelein, Robert A.
# TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMMLIAN PROTEINS
# NUMBER OF SEQUENCES: 11
# CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                 512 -----LEEQKELHYASLSFSEMK----SREPKDQEAPSTTEYSEIK 548
                                                                                                                                                                                                                                                                                                479 ED------PIMGTITSGSRKKPWPDSPGDQASPPGDAPP-----
                                                                                                                                                                                                                                                                                                                                           593 SSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQA----DYAEVK 637
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FILLING DATE: US/08/759,628
FILLING DATE: 05-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5e-58
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41.2%; Pred. No. 5e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 05-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,574
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/08759628 Patent No. 6225446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 901 California Avenue
Palo Alto
California
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TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 amino acids
amino acid
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Best Local Similarity 41.2's
Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ching, Edwin P. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94304-1104
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TELEFAX: 4
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3 LPLLLSSLL-GGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWF 61

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121 RGRDVKYSYQQNKINLEVTALIBKP-------DIHLSGP------ 152
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                                                                                                           61 RDGBIPYYAEVVATNNPDRRVKPETQGRFRLLGDVQKKNCSLSIGDARMEDTGSYFFRVE 120
                                                                                                                                                            122 RGSYVRYNFMNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPR 181
                                                                                                                                                                                                                                                                          182 DLVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQ----PPATLSWVLQNRVL 237
                                                                                                                                                                                                                                                                                                                                                                                                                           185 AXSARWIPRPXAPRELILIPRPEDHGINLICQMK-RQGAQVITEXTVQLAVSYAPQTIII 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     352 LELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQAS 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 LELRRVRSAEEGGFTCRAQHPLGFLQIFLNLSVYSLPQLLGPSCSWEAEGLHCRCSFRAR 360
                                                                                                                                                                                                                                                                                                                                                                                  238 SSSHPWGPRPLG---LELPGVKACDSGRYTCRAENRLGSQ---QRALDLSVQYPPENLRV 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          292 MVSQANRTVLENLGNGTSLPVLEGGSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGV 351
1 MPLLLLPLLWGGSLQEXPVYELQVQKSVTVQEGLCVLVPCSFSYPWRSWYSSPPLYVYWF 60
                                                       62 KAVTETTKGAPVATNHOSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVE
                                                                                                                                                                                                                                                                                                                        -----LESGLWRPTRLSCSLPGSCVAGPPLTFSWTGN----
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APPLICANT: ERICKSON-MILLER, CONNIE
TITLE OF INVENTION: Staloachesin Family Member-2
TITLE OF INVENTION: (SAF-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAPSLCWRLDEKPLEGNSSQGSFKVNSSSAXP 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 412 PAPSLRWWLGEELLEGNSSQDSFEVTPSSAGP 443
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APPLICATION NUMBER: US/09/038,832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MBER: US/09/038,832
11-MAR-1998
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/041,886
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09038832
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STREET: P.O. BOX 980
CITY: VALLEY FORGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23,031
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REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
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IBM Compatible
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610-407-0701
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6146845
GENERAL INFORMATION:
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161

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61 PVHGYWFRAGDRPYQDAPVATNNPDREVQAETQGRPQLLGDIWSNDCSLSIRDARKRDKG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   272 GSQQRALDLSVQYPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPAR 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----LDVSYPPWNLTMTVFQGDATASTALGNGSSLSVLEGQSLRLVCAVNSNPPAR 292
                                                                                                                                                                                                                                                                                                                          162 SRK-----GVSAQRTVRLRVAYAPRDLVISISRDNTPALBPQPQGNVPYLEAQKG
                                                                                                                                                                                                                                                                                                                                                                                  55 PAYGYWFKAVTETTKGAPVATNHQSREVEMSTRGRPQLTGDPAKGNCSLVIRDAQMQDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 QYFFRVERGSYVRYNFMNDGFF----LKVTVLSFTPRP------QDHNTDLICHVDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 ACKOGTPPMISWIGASVS-----SPGP---TTARSSVLTLTPKPODHGTSLTCO--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----VTLPG--TGVTTTSTVR----
                                                                                                                                                                                                                                                                                              1 MLLPLLLSSLLGGSQAMDG-----RFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              332 LSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSV 384
                                                                                                                                                                                                                                                     97;
                                                                                                                                                                                                               Length 431;
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Patent No. 6090582

GENERAL INFORMATION:

APPLICANT: KIKLY, KRISTINE

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSER: Ratner & Prestia

STREET: P.O. Box 980

CITY: Valley Forge
                                                                                                                                                                                                          Query Match
19.8%; Score 667.5; DB 3;
Best Local Similarity 39.2%; Pred. No. 7.9e-49;
Matches 162; Conservative 52; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPENATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,736
FILING DATE: 24-MAR-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/041,885
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                    LENGTH: 431 maino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-038-832-4
TELEX: 846169
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 431 amino acid
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                                                                                                                                                                                                                                                                                              PVHGYWFRAGDRPYQDAPVATNNPDREVQAETQGRFQLLGDIWSNDCSLSIRDARKRDKG 120
                                                                                                                                                                                                                                                                                                                                                                       121 SYFFRIERGS-MKWSYKSQLNYKTKQLSVFVTALTHRPDILILGTLESGHSRNLTCSVFW 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 -----LDVSYPPWNLTMTVFQGDATASTALGNGSSLSVLEGQSLRLVCAVNSNPPAR 292
                                                                                                                                                                                                                                                          PAYGYWFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDES 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 ACKQGTPPMISWIGASVS-----SPGP---TTARSSVLTLTPKPQDHGTSLTCQ-- 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QFLRLLCAADSQPPATLSWVLQNRVLSSSHPWGPRPLGLELPGVKAGDSGRYTCRAENRL 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        272 GSQQRALDLSVQYPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPAR 331
                                                                                                                                                                                                                                                                                                                                              115 QYFFRVERGSYVRYNFMNDGFF----LKVTVLSFTPRP------QDHNTDLTCHVDF 161
                                                                                                                                                                                                                                                                                                                                                                                                                                  SRK------GVSAQRTVRLRVAYAPRDLVISISRDNTPALEPQPQGNVPYLEAQKG 211
                                                                                                                                                                                                                 1 MLLLLLLLPLLWGTKGMEGDRQYGDGYLLQVQELVTVQEGLCVHVPCSFSYPQDGWTDSD 60
                                                                                                                                                                        1 MLLPLLLSSLLGGSQAMDG-----RFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGST
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                                                                                                                                 Gaps
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|SWTRGSLTLCPSRSSNPGLLELPRVHVRDEGEFTCRAQNAQGSQHISLSLSL 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332 LSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSV 384
                                                                                    ; Score 667.5; DB 3; Length 431;
; Pred. No. 7.9e-49;
52; Mismatches 102; Indels 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09038832
Patent No. 614845
GENERAL INFORMATION:
APPLICANT: KIKLY, KRISTINE
APPLICANT: ERICKSON-WILLER, CONNIE
TITLE OF INVENTION: (SAF-2)
NUMBER OF SQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAINER & PRESTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
COMPUTER: IBM COMPATIBLE
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 11-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRICE APPLICATION DATA:
APPLICATION NUMBER: 60/041,886
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTATA, PALL F.
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-50018
TELECOMUNICATION INFORMATION:
TELECHONE: 610-407-0701
                                                                                      Query Match
Best Local Similarity 39.2%;
Matches 162; Conservative 52
  ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-038-832-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: P.O. BOX 980
CITY: VALLEY FORGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 19482
COMPUTER READABLE FORM:
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US-09-038-832-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169 QRTVRLRVAYAPRDLVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 SWVLONRVLSSSHPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPEN 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----TINKTIQINVSYPPON 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  289 LRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSD 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 LIVIVFQGEGTASTALGNSSSLSVLEGGSLRLVCAVDSNPPARLSWIFWRSLTLYPSQPSN 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         349 PGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSV--HYSPKLLGPSCSWEAEGLHCSC 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             407 SSQASPAPSLRWWLGEELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAW 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   467 NVHGAQSGSILQLPDKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETP 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GAVGGAGATALVFLSFCVIFIVV---RSCRKKSA 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       527 RPRFSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLP 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 AYGYWFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VHGYWFRAGNDISWKAPVATNNPAWAVQEETRDRFHLLGDPQTKNCTLSIRDARMSDAGR
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
18.5%; Score 626; DB 3; Length 467;
Best Local Similarity 28.6%; Pred. No. 3.3e-45;
Matches 186; Conservative 79; Mismatches 184; Indels 202; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 LIPLILISSILGGSQAMDGR----FWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----VTLPGAGV-----
REGISTRATION NUMBER: 23,031
REFRENCE/DOCKET NUMBER: GH-50019
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
                                                                                                   TELEFAX: 610-407-0701
                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                           linear
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169 SWMSAAPHILGPRITQSSVLTITP-AQDHSTNLTCQVTFPGAGVIMERTIQLNVSYAPQK 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 WGPRPLGLELPGVKAGDSGRYTCRAENRLGSOORALDLSVOYPPENLRVMVSOANRTVLE 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 LVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----ILONT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 WF-----LEGADVPVATNDPDEEVQEETRGRFHLLWDPRRKNCSLSIRDARRRDNAAYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 FRL-KSKWMKYGYTSSKIYVRVMALTHRPNISIPGPGVWPSSNLTCSVPWVCEQGTPPIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       303 NLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 LLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSF--SYPRQDWTGSTPAYGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MIPLILIPLIMAGALAQERRPOLEGPESLTVQEGLCVLVPCRLPTTLP----ASYYGYGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 317;
INVENTION: MUTATIONAL VARIANTS OF MAMMLIAN PROTEINS SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 440;
                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,628
FILING DATE: 05-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.4%; Score 586.5; DB 3; 24.7%; Pred. No. 7.4e-42; sive 73; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06 60/008,574
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0552Q
TELECHNINICATION INFORMATION:
TELEPHONE: 415-496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 FRVERGSYVRYNFMNDGFFLKV-----
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                                                                                            3: DNAX Research Inst
901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228 VAISIFOGNSAAFK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 24.7
Matches 172, Conservative
                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
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                                                                                                                                                                            California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                               CITY: Palo Alto
STATE: Californi
COUNTRY: USA
                                                                                                                                                                                                                       94304-1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 05 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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---WKPEG---

Altmann, Scott W. Rock, Fernando L. Bazan, J. Fernando Kastelein, Robert A.

APPLICANT: APPLICANT: APPLICANT: APPLICANT:

Sequence 4, Application US/08759628 Patent No. 6225446 GENERAL INFORMATION:

US-08-759-628-4

RESULT 6

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61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 GEGTASTALGNSSSLSVIEGGSLRLVCAVDSNPPARLSWTWRSLTLYPSGPSNPLVIEL- 215
                                                                                                                                                                                                                                                                                                               RVQVEHEGEFTCHARHPLGSQHVSLSLSV--HYSPKLLGPSCSWEAEGLHCSCSSQASPA 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       474 GSILQLPDKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRH 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ...----AADVGDIGMK-------DANTIRGSASQGNLTESWADDNPRH 328
                                                                                                                                                                                                                                        296 ANRIVLENLGNGTSLPVLEGOSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELP 355
              116 YFFRVERGSYVRYNFMNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLR 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MPLILLLEPILMAGALAMDPNFWLQVQESVTVQEGLCVLVPCTFFHPIPYXDKNSPVHGYW 60
                                                                                    176 VAYAPRDLVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNR
                                                                                                                                                                                        414 PSLRWWLGBELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          257 GVLL------GAVGGAGATALVFLSFCVIFIVV---RSCRKKSARP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                534 STILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MILPLILSSILGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
                                                                                                                                                                236 VLSSSHPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  329 HGLAAHSGEEREIQYAPLSFHKGEPQ-DLSGQEATNNEYSEIK 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            594 STQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK
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                                                                                                                                                                                                                                                                                                                                         Query Match 13.3%; Score 448.5; DB 4;
Best Local Similarity 21.4%; Pred. No. 3.9e-30;
Matches 149; Conservative 48; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ni, Jian
APPLICANT: Gentz, Reiner L.
APPLICANT: Gentz, Craig A.
TITLE OF INVENTION: CD33-Like Protein
FILE REFERENCE: 1488.048001.
FULR REFERENCE: 1488.048001.
CURRENT PEDLICATION NUMBER: 050022,481
PRIOR PILING DATE: 1996-07-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SED ID NO: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08896537A, Patent No. 6590088, GENERAL INFORMATION:
                                      ||||:|:|: :::|: |
| YFFRMEKGN-IKWNYKYD-----
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-896-537A-3
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                                                                                                                                                                                        ----SRGHQHQFQTGIVSDHPAEAGPISE 406
                                        -----RAGGVL---- 335
                                                                                                              -----GAVWGASİTTLVFLCVCFİF------RVKTRKKKQPSQCKXTDDVNP 376
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ELLEGNSSODSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAOSGSILOLPDK 482
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                                                                          483 KGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 15.8%; Score 532.5; DB 3; Length 374; Best Local Similarity 25.2%; Pred. No. 2.5e-37; Matches 162; Conservative 64; Mismatches 137; Indels 281;
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KIKLY, KRISTINE
APPLICANT: ERICKSON-MILLER, CONNIE
TITLE OF INVENTION: Staloadhesin Family Member-3
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                         ::||||| |:|||| DEQELHYAVLHFHKVQPQE----PKVTDTEYSEIK 437
                                                                                                                                                                                                                              603 SQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK 637
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,736
FILING DATE: 24-MAR-1998
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 24-MAR-1998
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/041,885
FILING DATE: 02-ARR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
TELECONMUNICATION INFORMATION:
TELECONMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09046736 Patent No. 6090582 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
                                                                                                                                                                                          377 VMVSG------
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          374 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 610-407-0701
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TOPOLOGY: linear
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OPERATING SYSTEM:
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109 LESHCAAARDTVQCLCVVKSNPEPSVAFELPSRNVTVNETEREF-VYSERSGLLLTSILT 16 451 LHGGLSSGLRLRCEAMVVHGAQSGSILQLPDKKGLISTAFSNGAFLGIGITALLF 50	CY 506 LCLALIMKILPKRRTQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTP 565 CY 506 LCLALIMKILPKRRTQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTP 565 Db 216 ALLIAIVYITQTRRKKQVTESPSFSAG	RESULT 10 US-08-05-31 JSGGROGE 31, Application US/08408095 JSGGROGE 31, Application US/08408095 JSGGROGE 31, Application US/08408095 JSGGROWATION JETLE OF INVEXATION: APPDTOPSIS-REGULATING PROTEINS NUMBER OF SEQUENCES: 35 CORRESPONDENCE ADDRESS: 35 CORRESPONDENCE ADDRESS: 35 CORRESPONDENCE ADDRESS: 36 CORRESPONDENCE ADDRESS: 36 COUNTRY: USA ZIP: 2003 Peansylvania Avenue, N.W. STREET: 100 Peansylvania Avenue, N.W. STREET: 2004 Peansylvania Avenue, N.W. STREET: 2004 Peansylvania Avenue, N.W. COMPUTER: IBP Compatible COMPUTER: IBP COMPATIBLE COMPATIBLE COMPUTER: IBP COMPATIBLE COMPUTER: IBP COMPATIBLE COMPUTER: IBP COMPATIBLE COMPATIBLE COMPUTER: IBP COMPATIBLE COMPUTER: IBP COMPATIBLE	Query Match Best Local Similarity 20.8%; Score 230.5; DB 2; Length 501; Best Local Similarity 20.8%; Pred. No. 3.3e-11; Matches 138; Conservative 66; Mismatches 219; Indels 239; Gaps 29; Qy 24 RVQESVWAVPEGLCISVPCSFSYPRQDWTGSTPANGYWFKAVTETTKQAPVAIN 76	Db 30 RTEEKVHIPKILPWHAGTYSCVAENILGTGQRGPGAELDVQ 70 Qy 77 HQSREVEMSTRGRFQL-TGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYVRXNFWNDGF 135	Db 71 YPPKKVTTVIQNPMPIREGDIVTLSCNYNSSNPSVTRYEWKPHGA 115 Qy 136 FLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVISIS 188 Db 116 WEEFSLGVLKIQNVGWDNTTIACARCNSWCSWASPVALNVQXAPRDVRVRKI 167
IFSW 17 RDLV 18	00 185 ISISEDNTPALEPQPQGNUPYLEAQKGGFLRLCAADSQPPATLSWULQURVLSSSHFWG 244 236	99 364 EFTCHARHPLGSQHVSLSLSVHYSPKLLGPSCSGREAGGLHCSCSSQASPAPSLRWMLGEE 423 126	, LENGTH: 318 5242798-5 Query Match 7.0%; Score 237.5; DB 6; Length 318; Best Local Similarity 25.1%; Pred: No. 4.2e-12; Matches 95; Conservative 60; Mismatches 146; Indels 77; Gaps 13;	QY 272 GSQQRALDISVQYPPENLRVMVSQANRTVLENLGNGTSLPVLEGGSLCLVCVTHSSPPAR 331	QY 332 LSWTQRQQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSGHVSLSLSVHYSPKLL 391

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Chicago
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STATE: Il
COUNTRY:
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RDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLS--WVLQNRVLSSSHPWGPR 246
                                                              PLGLELPGVKAGDSGRYTCRAENRLG-SQQRALDLSVQYPPENLRVMVSQANRTVLENLG 305
                                                                                                                              306 NGTSLPVLEGOSLCLVCVTHSSPPAR----LSWTQRGQVLSPSQPSDPGVLELPRVQVEH 361
                                                                                                                                                                                                                                                             411 SPAPSLRW--WLGEELLEGNSSQDSFEV-----TPSSAGPWANSSLSLHGGLS----S 457
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                                                                                          210 ---LNFDSISPEDAGSYSCWVNNSIGOTASKAWTLEVLYAPRRLRVSMSPGDQ-----
                                                                                                                                                                                                                                                                                                                              GLRLRCEAWNV--HGAQSGSILQLPDKKGLISTAFSNGAFLGIGITALLFLCLALIIMKI
                               K-----PLSEIHSGNSVSLQCDFSSSHPKEVQFFWEKNGKLLGKESQ---
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APPLICANT: Kilgannon, Patrick D.
TITLE OF INVENTION: ICAM-4 Materials and Methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
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FILING DATE: 27-JAN-1992
ARIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5700658
GENERAL INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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PRIOR APPLICATION DATA:
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US-08-245-295-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 LTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYVRYNFMNDGFFLKVTVLSFTPRPQDH 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267 AENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHS 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 PEGLCISVPCSFSYPRODWIGSTPAYGYWFKAVTETIKGAPVAINHOSREVEMSTRGRFQ 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49; Mismatches 146; Indels 144;
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1.1e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 229;
Pred. No. 1
APPLICATION NUMBER: US 08/009,266 FILING DATE: 22-JAN-1993 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852 FILING DATE: 05-AUG-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             United States of America
                                                                                                                ATCHEY/AGENT INPURMALLANDRAME:
NAME: BORUN, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 2786/
TELEPROMUNICATION INPORMATION:
TELEPROMUNICATION INPORMATION:
TELEPROM: 312-474-0448
TELER: 25-3856
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 917 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.8%;
Best Local Similarity 24.8%;
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// MOLECULE TYPE: protein
US-08-245-295-2
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TELECOMMUNICATION INFORMATION:
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELEFAX: 3
                                                                                                                                                           RESULT 13
US-08-656-984A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              519 VPPPSVSCVRSGK-----EBVMEGPLRVAREHAGTYRCEAINARGSAAKNVAVTVE 569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 PEGLCISVPCSFSYPRQDWTGSTPAYGYWFKAVTETTKGAPVATNHQSREVEMSTRGRFQ 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               335 PEGKMYTVSC-----WAGA------RALV-TLEGIPAAVPGQPAELQLN----
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DCS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                            PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-DAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION NUMBER: US 08/245,295
FILING DATE: 18-MAY-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
                                                                                                                                 APPLICATION NUMBER: US/08/481,130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: WILLIAMS, JR. JOSEPH A. REGISTRATION NUMBER: 38,659 REFERENCE/DOCKET NUMBER: 27866 TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 25-3856
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 917 amino acids
TYPE: amino acid
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570 YGPSFEELGCPSNWTWVEGSGKLFSCEVDGKPEPRVE-CVGS---EGASEGVVLPLVSSN 625
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Best Local Similarity 24.8%; Pred. No. 1.1e-10;
Matches 112; Conservative 49; Mismatches 146; Indels 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: Marshall, O'Toole, Gerstein, Murray & Borun
233 South Wacker Drive, 6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gallatin, W. Michael
APPLICANT: Kilgannon, Patrick D.
TITLE OF INVENTION: ICAM-4 Materials and Methods
NUMBER OF SEQUENCES: 42
CORRESSEDNOMENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/656,984A
                                                                                                                                441 AGPWANSSLSLHGGLSSGLRLRCEAWNVHGA 471
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PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/827,689
FILING DATE: 27-3An-1992
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/894,061
FILING DATE: 05-UN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 05-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/245,295
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COUNTRY: United States of America
ZIP: 66605-6405
COMPUTER READABLE FORM:
MEDIUM TYPER: Floppy disk
COMPUTER: IRW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: US 08/485,604
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
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18-MAY-1994
                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08656984A
Patent No. 5753502
GENERAL INFORMATION:
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                                                                                                                                            152 NTDLICHVDFS--RKGVSAQRIVRLRVAYAPR--DLVISISRDNTPALEPQPQGNVPYLE 207
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                                                                       92 LTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYVRYNFMNDGFFLKVTVLSFTPRPQDH 151
PEGLCISVPCSFSYPRODWTGSTPAYGYWFKAVTETTKGAPVATNHQSREVEMSTRGRFQ 91
                              ----RALV-TLEGIPAAVPGOPAELQLN----
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                                                                                                        ------VIKNDDKRGFF
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08485604
Parent No. 5773293
GENERAL INFORMATION:
APPLICANT: WP, W. Michael
APPLICANT: Kigannon, Patrick D.
TITLE OF INVENTION: ICAM-4 Materials and Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murrav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 471
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APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-0AN-1992
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
RICH APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
                                    PEGKMVTVSC-----WAGA--
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STREET: 250
TW: Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPPARLSWIQRGQVLSPSQPSDPGVLELP-RVQVEHEGEFTCHARHPLGSQHVSLSVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 PEGLCISVPCSFSYPRQDWTGSTPAYGYWFKAVTETTKGAPVATNHQSREVEMSTRGRFQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 IIGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYVRYNFWNDGFFLKVTVLSFTPRPQDH
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                                                                                                                                                                                                                                                                                                                                                                                                            6.8%; Score 229; DB 1; Length 917; 24.8%; Pred. No. 1.1e-10;
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             PRIOR APPLICATION DATE:
APPLICATION UNBER: US 08/245,295
FILING DATE: 18-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, UR. OOSEPH A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32715
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          States of America
05-AUG-1993
                                                                                                                                                                                                                                                                                      : 917 amino acids
amino acid
                                                                                                                                                                                                                         TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 24.8 Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                  linear
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COUNTRY: United
ZIP: 60606-6402
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US-08-487-595-2
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335 PEGKMVTVSC-----WAGA-----RALV-TLEGIPAAVPGQPAELQLN----- 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 NTDLTCHVDFS--RKGVSAQRTVRLRVAYAPR--DLVISISRDNTPALBPQPQGNVPYLE 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       383 -CDAALDVDGETLRKNQSSE----LRVLYAPRLDDL------DCPRSWTWPEGPEGTLH 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----CEARGNPEPS-----VHCARPDGGAVLALGLLGPVTRALAGTYRCT 471
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24.8%; Pred. No. 1.1e-10;
trive 49; Mismatches 146; Indels 144; Gaps
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              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,595
FILNG DATE: PATENTION: 435
PRIOR APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: WILLIAMS, JR. JOSEPH A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32714
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/245,295
FILING DATE: 18-MAY-1994
TIORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 24.8%
Matches 112; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
COMPUTER READABLE FORM:
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570 YGPSFEELGCPSNWTWVEGSGKLFSCEVDGKPBPRVE-CVGS---EGASEGVVLPLVSSN 625
                                                                                               SG--SRNSMT-PGNLSPGIYL-CNATWRHGS 652
                                                441 AGPWANSSLSIHGGLSSGLRIRCEAWNVHGA 471
                                                                                                                                                                 Search completed: November 5, 2004, 13:58:25 Job time: 25.6516 secs
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; Search time 74.3927 Seconds (without alignments) 3081.324 Million cell updates/sec
                                                                                                                                                                                      1 MLLPLLLSSLLGGSQAMDGR.....RPEARMPKGTQADYAEVKFQ 639
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                     2002273 segs, 358729299 residues
                                                                                            5, 2004, 13:50:17
                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           geneseqp2003as:*
geneseqp2003bs:*
geneseqp2004s:*
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Gapop 10.0 , Gapext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                geneseqp2001s:*geneseqp2002s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   geneseqp1980s:*
geneseqp1990s:*
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Maximum DB seq length: 200000000
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3377
                Copyright
                                                                                            November
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                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                                      Scoring table:
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                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                       Searched:
                                                                                            Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aaw81023 Human sia	m	Aab25580 CD33-like	052	582	87	153	Add26582 Siglec-10	0	'n	Aau87075 Sialic ac	4,	Aau87074 Sialic ac	Aay41724 Human PRO	Aab44280 Human PRO	2 Human	Abu58458 Human PRO	Abu88006 Novel hum	Abu84321 Human sec	Abr66195 Human sec	Abr65585 Human sec	9525 Human	Abu82764 Human PRO	Abu89885 Novel hum	Abr68134 Human sec
SUMMARIES	ID	AAW81023	AAY97543	AAB25580	ADA27052	ADE86582	AAU87087	ADA27153	ADD26582	AD137010	ADL82805	AAU87075	ADD19314	AAU87074	AAY41724	AAB44280	AAU29082	S	О	ABU84321	ABR66195	Φ	ABU99525	ABU82764	988	ABR68134
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	Score	3377	3377	3354	3354	3354	3338	m	33	33	m	3299	7	803.	2790.5	ö	790.	79	790.	79	790.	90.	790.	790.	2790.5	2790.5
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Abu96187 Novel hum	Abu92618 Human sec	Abo08695 Human sec	Human	Abr74901 Human sec	Human	Novel	Abu85636 Human PRO	Novel	1 Novel	Novel	Novel	Abu89410 Human PRO	Abu86251 Human sec	Abu67464 Human sec	Abu80492 Human PRO	Abr99410 Human sec	Abr98800 Human sec	Abo16323 Human sec	Abr92223 Human sec
5 ABU96187		5 ABO08695	5 ABO02747	5 ABR74901	5 ABR94663	5 ABO25226	5 ABU85636	5 ABU98796	5 ABU98011	5 ABU91717	5 ABU72232	5 ABU89410	5 ABU86251	5 ABU67464	5 ABU80492	5 ABR99410	5 ABR98800	5 ABO16323	5 ABR92223
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82.6	82.6	82.6	82.6	82.6	82.6	82.6	82.6	82.6	82.6	82.6	82.6	82.6	82.6	82.6	82.6	82.6	82.6	82.6	82.6
2790.5	2790.5	2790.5		2790.5	2790.5	2790.5	2790.5	-	2790.5	2790.5	2790.5	2790.5	2790.5	2790.5	2790.5	2790.5	2790.5	2790.5	2790.5
							33					38	39	40	41	42	43	44	45

ALIGNMENTS

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This is the amino acid sequence of new human sialoadhesin family 4 (SAF-4), as deduced from the nucleotide sequence of an isolated cDNA clone (see AAV99911). SAF-4 polynucleotides and polypeptides, and methods for producing such polypeptides in transformed host cells using recombinant techniques are disclosed. SAF-4, its agonists and antagonists, and nucleat acid molecules that enhance or inhibit SAF-4 expression, may be used to treat patients in need of enhancement or inhibition of SAF-4
                                                                                                                                                       SAF-4; staloadhesin family; human, therapy; diagnosis; cancer; inflammation; autoimmune disease; allergy; asthma; inflammation; cerebellar degeneration; Alzheimer's disease; Parkinson's disease; multiple sclerosis, amyotrophic lateral sclerosis; head injury; septic shock; sepsis; stroke; osteoporosis; osteoparthritis; lischemia reperfusion injury; cardiovascular disease; kidney disease; liver disease; myocardial infarction; hypotension; hypertension; AIDS; myelodysplastic syndrome; aplastic anaemia; baldness; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New sialoadhesin family 4 polypetides and polynucleotides treat various diseases associated with SAF-4 expression.
                                                                                                                      Human sialoadhesin family 4 (SAF-1) polypeptide.
               AAW81023 standard; protein; 639 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 31; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Erickson-Miller CL;
                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US010791,
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                                                                                     (first entry)
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N-PSDB; AAV99911.
                                                                                                                                                                                                                                                                                                                                                                                                                                        27-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                  409853840-AL
                                                                                     26-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                       03-DEC-1998.
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                                                    AAW81023;
AAW8102
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to

us-09-937-636-4.nov04.rag

Human obesity protein binding protein-2 homologue; hOB-BP2h; obesity; obesity;

Human obesity protein binding protein-2 homologue

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expression or activity. Conditions that may benefit from such treatment include cancer, inflammation, autoimmunity, alleay, satisfua, rheumatoid arthritis, CNS inflammation, cerebellar degeneration, Altheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, head injury damage and other neurological disorders, septic shock, sepsis, stroke, osteoporosis, osteoathritis, ischemia reperfusion injury avocardial infarction, hypotension, hypertension, Albs. myelodysplastic syndromes and other heamatologic abnormalities, aplastic anaemia, male baldness pattern and bacterial, protozoal, fungal and viral infections related to SAF-4 polypeptide activity, Methods of identifying agonists, anatagonists/inhibitors are also provided, as well as diagnostic assays for detecting diseases associated with inappropriate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MLLPLLESSLLGGSQAMDGRFWIRVQESVMVPBGLCISVPCSFSYPRQDWTGSTPAYGYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ERGSYVRYNFWNDGFFLKVTVLSFTPRPQDHNTDLICHVDFSRKGVSAQRTVRLRVAYAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 HPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVWVSQANRTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 HPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ERGSYVRYNPMNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RDLVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 RDLVISISRDNTPALEPOPPOGNVPYLBAOKGOFLRLLCAADSOPPATLSWVLONRVLSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                         Length 639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 3377; DB 2;
100.0%; Pred. No. 2.3e-232;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 639; Conservative
                                                                                                                                                                                                                                                                                                                  SAF-4 activity or levels
                                                                                                                                                                                                                                                                                                                                                             Sequence 639 AA;
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୍ର ବ୍ୟୁ କ୍ରହ୍ମ କ୍ରହ୍ମ କ୍ରହ୍ମ କ୍ରହ୍ମ କ୍ରହ୍ମ କ୍ରହ୍ମ କ୍ରହ୍ମ କ୍ରହ୍ମ କ୍ରହ୍ମ କ୍ରହ୍ମ କ୍ରହ୍ମ କ୍ରହ୍ମ କ୍ରହ୍ମ କ୍ରହ୍ମ କ୍ରହ
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New human obesity protein binding protein-2 homologue nucleic acids, polynucleotides and polypeptides useful for producing medicament for treating obesity and/or obesity-related disorders.

99US-0127667P

02-APR-1999;

(ELIL) LILLY & CO

Wei J;

Su EW,

N-PSDB; AAA37848

22-MAR-2000; 2000WO-US006682

WO200059942-A2

Homo sapiens

Claim 9; Page 89-91; 92pp; English

This sequence is a human obesity protein binding protein-2 homologue (hobbe used for the manufacture of a medicament for the treatment of obesity and/or obesity-related disorders. The hob-BP2h nucleic acids are useful as probes or amplification primers in the detection, quantification or isolation of gene sequences or transcripts, for recombinant expression of hob-BP2h polypeptides, as immunogens in the preparation and screening of antibodies, and in sense or antisense suppression of one or more hob-BP2h antiponic epitope-bearing peptides and of one or more hob-BP2h Antigenic epitope-bearing peptides and oplypeptides are useful for a singing of screening antibodies that specifically binds to the hob-BP2h 120 120 180 180 240 240 300 9 9 ERGSYVRYNFWNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP LENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVE LENLGNGTSLPVLEGGSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVE FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV ERGSYVRYNFMNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP HPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTV 1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW 1 MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW RDLVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSS 181 RDLVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSS 241 HPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTV FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV Gaps 0: Length 639; Indels 100.0%; Score 3377; DB 3; 100.0%; Pred. No. 2.3e-232; iive 0; Mismatches 0; Query Match Best Local Similarity 100. Matches 639; Conservative Sequence 639 AA; polypeptides 19 19 121 121 181 301 ò g 염 ò g 임 à ò 9 Š ð

> 360 360

LENLGNGTSLPVLBGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLBLPRVQVB

301

DD

301 LENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVE

HEGEFTCHARHPLGSQHVSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPAPSLRWWL 361 HEGBFTCHARHPLGSQHVSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPAPSLRWWL GEELLEGNSSODSFEVTPSSAGFWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGSILQLP

361

ò 셤

420

420

540

600 600

541 NVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPES

QESQEELHYATINFPGVRPRPEARMPKGTQADYAEVKFQ 639

AAY97543 standard; protein;

RESULT 2 AAY97543

(first entry)

12-FEB-2001

AAY97543;

SXE

QESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ

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GEBLILEGNSSODSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGSILQLP

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DKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRIQTETPRPRFSRHSTILDYI 541 NVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPES HEGEFTCHARHPLGSQHVSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPAPSLRWWL 420

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The present invention relates to 12 secreted human proteins and the nucleotide sequences encoding them. The polynucleotide sequences given in AAA80606-A80623 encode the 12 secreted protein sequences given in AA825576-B25593. The human secreted proteins have various activities dependent on the tissues in which they are expressed. Examples of the activities of the proteins include: immunosuppressant; anti-inflammatory, antiarthritic; antirheumatic, dermatological; antiproliferative; antiarteriosclerotic; anticoncer, vulnerary, antivital; antibacterial; and antifungal activity. The proteins, polypeptides, agonists and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic; antiaumunatic, dermatological; antiprollferative; antiarteriosclerotic; anticancer; vulnerary; antiviral; antibacterial; antifungal; immune disorder; Addison's disease; rheumatoid arthritis; dermatitis; multiple sclerosis; inflammatory disorder; inflammatory bowel disease; Crohn's disease; nephritis; hyperprollerative disorder; cancer; cardiovascular disorder; concary arteriosclerosis; myocarditis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acid molecules encoding human secreted proteins are u for the prevention, amelioration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, cancer, wounds, and infectious diseases.
HEGEFTCHARHPLGSQHVSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPAPSLRWWL
                                                                                                                                                                                                                            NVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSPPEPKSSTQAPES
                                                     GEELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGS1LQLP
                                                                                      GEELLEGNSSODSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGSILQIP
                                                                                                                         DKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYI
                                                                                                                                                      DKKGLISTAFSNGAFLGIGITALLFLCLALIMKILPKRRTQTETPRPRFSRHSTILDYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD33-like protein encoded by human secreted protein gene #5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   melanoma; lymphoma; wound healing; human.
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antagonists may be used to treat prevent and/or diagnose various disease, Addisorders and conditions examples of which include: immune disorders e.g. Addisorder disease, rheumatoid arthritis, dermatitis, and multiple sclerosis; inflammatory disorders e.g. inflammatory bowel disease, Crohn's disease and nephritis; hyperproliferative disorders such as paraptroleniamemias and purpura; cardiovascular disorders e.g. coronary arteriosclerosis and myocarditis; cancer e.g. melanoma and lymphoma. The proteins and polynucleotide sequences may also be used in wound healing and the treatment of infectious diseases. The human secreted protein gene #5 and protein sequences are represented in sequences AAA80610 and AAB25580. Sequences AAA80619 represent genes related to the
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Pred. No. 1e-230;
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hemostatic, gene therapy, cancer, inflammation, immune disorder, neurological disorder, blood clotting disorder, food additive, preservative, human, secreted protein.
cytostatic; antiinflammatory; immunomodulator; neuroprotective;
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US2003055231-A1

20-MAR-2003

2001US-00984130 29-OCT-2001;

27-OCT-1999; 99WO-08025031. 19-APR-2000; 2000US-0198407P. 30-OCT-2000; 2000US-0243792P. 18-APR-2001; 2001US-00836353. 28-OCT-1998;

(NIJJ/) (YOUN/) (KENN/)

NI J. YOUNG P E. KENNY J J. OLSEN H S. MOORE P A. (OLSE/) (WEIY/)

LIU D. CROCKER P R GREENE J M. RUBEN S M. (GREE/) (RUBE/) (LIUD/) (CROC/) Kenny JJ, Olsen HS, Crocker PR; Young PE, M, Liu D, Ruben SM,

Greene JM;

>-Wei

Moore PA,

WPI; 2003-567103/53. N-PSDB; ADA27034.

New human secreted nucleic acid molecules and polypeptides, useful for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation, immune disorders, neurological and blood clotting disorders.

Claim 11; Fig 13; 454pp; English.

The invention relates to an isolated nucleic molecule that is at least 55% identical to 19 human cDNA sequences representing 12 novel genes 50% identical to 19 human cDNA sequences representing 12 novel genes 50% identical to 19 human cDNA sequences representing 12 novel genes 50% identical sequence contained in American Type Culture Collection (ATCC) deposit No. defined in the specification, its species homologue, a variant or allelic correction of the polymoclectide having a polymuclectide having a polymuclectide having a polymuclectide are the polymoclectide are compinant vectors, host cells (for producing the polypeptide), the recombinant vectors, host cells (for producing the polypeptide), the secreted polypeptide (comprising a sequence that is at least 95% incention to a polypeptide (for producing the polypeptide), antibodies that secreted polypeptide (for producing the polypeptide), antibodies that content variant, allelic variant or species homologue), antibodies that spretchin variant, allelic variant or species homologue), antibodies that spretchin and to the polypeptides, diagnosing, treating, preventing or ameliorating a medical condition by administering the polypeptides are sequence in a cell, isolating the supernatant, and detecting an activity in a biological sasay and identifying the protein in the supernatant of naving the activity). The polypeptides, nucleic acids and antibodies are cuseful for diagnosing a pathological condition or a susceptibility to a pathological condition, for preventing, treating, or ameliorating a pathological condition and other immune content and pathological and blood clotting disorders (many examples are disorders, neurological and blood clotting disorders (many examples are disorders, neurological and blood clotting disorders (many polypeptides and antibodies are also useful for chromosome identification). The molypeptides and antibodies are useful for chromosome identification, radiation hybrid mapping are useful for tissues immunobistochemistry assays. The polyp

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agonist or antagonist may also be used as a food additive or preservative to increase or decrease storage capabilities, fat content or other nutritional components. The present is a secreted protein of the
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                                                                                                                   Query Match 99.3%; Score 3354; DB 6; 1
Best Local Similarity 99.5%; Pred. No. 1e-230;
Matches 636; Conservative 0; Mismatches 3;
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                                                                                     Sequence 639 AA;
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                                                      invention.
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The invention relates to an isolated SIGLEC (sialic acid-binding Igrelated lectin) protein [1]. Pharmaceutical compositions comprising [1] are useful for treating immune system diseases such as asthma, leukaemia or other allergic or inflammatory diseases such as asthma, leukaemia or or other allergic or inflammatory diseases. Extracellular domains of [1] represent potential markers for screening, disquosis, prognosis, follow up assays, and imaging methods. [1] is useful as a target for drugs which inflammation, tissue damage and remodeling in asthma, and inflammation tissue as allergic rhinitis, osteoarthritis, crohn's disease, psoriasis, rheumatoid arthritis, conjunctivitis, etc. [1] is also useful for monitoring the course of disease or disorders, and for identifying agents that bind with and/or modulate the biological activity of SIGLEC-BMS proteins. The nucleic acid molecules [1] encoding [1] are useful in diagnosis and/or prognosis methods, and to detect the presence and/or amount of SIGLEC-BMS nucleocids sequences and/or SIGLEC-BMS proteins in a biological sample. [11] are useful as nucleic acid probes are useful for screening genomic library to isolate a genomic clone of SIGLEC-BMS antibodies are also used to detect or isolate cells. The SIGLEC-BMS antibodies are also used to detect, sort or isolate cells
121 GEELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGSILQLP 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein molecules useful for treating immune system diseases such as asthma, leukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease.
                                        DKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYI
                                                                     541 NVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPES
                                                                                                                           NVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; sialic acid-binding Ig-related lectin; SIGLEC; asthma; mimune system disease; leuksemia; allergy; inflammatory disease; tissue damage; allergic rhinitis; osteoarthritis; Crohn's disease; psoriasis; rheumatoid arthritis; conjunctivitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sialic acid-binding Ig-related lectin, Siglec-BMS-L3-995-3.
                                                                                                                                                                                                            QESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ 639
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                                                                                                                                                                                                                                                                                                                                                              AAU87087 standard; protein; 697
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N-PSDB; ABK43373.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid sequence, or its allelic variant, a fragment of the cDNA sequence, or its fragment, domain, epitope or species homologue. The nucleic acid is useful for preparing a medicament for preventing, treating or ameliorating a medical condition e.g., cancer, liver disorders such as hepatitis or neural disorders such as Alzheimer's disease. The present sequence represents the amino acid sequence of a novel human secreted protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid molecule, useful for preparing a medicament for preventing, treating or ameliorating a medical condition e.g. cancer, liver disorders or neural disorders.
                                                                                                                                                                                                                                                                                                                                                              Greene JM;
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Pred. No. 1e-230;
0; Mismatches 3;
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                                                                              28-OCT-1998; 98US-0105971P.
27-OCT-1999; 99WO-US025031.
19-APR-2000; 2000US-0198407P.
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Best Local Similarity 99.5'
Watches 636; Conservative
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YOUNG P E.
KENNY J J.
OLSEN H S.
MOORE P A.
WEI Y.
GREENE J M.
RUBEN S M.
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N-PSDB; ADE86564.
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27-OCT-1999;
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expressing SIGLEC-BMS proteins and in diagnostic imaging technology. AAU87074-AAU87089 represent human SIGLEC amino acid sequences of the
                                                                                                                                        Indels 58; Gaps
                                                                                                      Length 697;
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                                                                                                        Score 3338; DB 5;
Pred. No. 1.6e-229;
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91.7%;
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Best Local Similarity 91.7
Matches 639; Conservative
                                                                      Sequence 697 AA;
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cytostatic; antiinflammatory; immunomodulator; neuroprotective; hemostatic; gene therapy; cancer; inflammation; immune disorder; neurological disorder; blood clotting disorder; food additive; preservative; human; secreted protein.
                                                                                                                                                                                                                                                           Human novel secreted protein from cDNA HDPCL05 #2.
ADA27153 standard; protein; 697 AA
                                                                                                                                                                       (first entry)
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20-NOV-2003

ADA27153;

ADA27153 RESULT

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The invention relates to an isolated nucleic molecule that is at least SX TA The invention relates to an isolated nucleic molecule that is at least CC 54 identical to 18 human CDNA sequences representing 12 novel genes encoding secreted proteins or a polymucleotide fragment of the CDNA contained in American Type Culture Collection (ATC) deposit No. defined in the specification, its species homologue, a variant or allelic variant of the polymucleotide having a polymucleotide agabale of hybridise under stringent conditions to a mucleic acid molecule des not hybridise under stringent conditions to a mucleic acid molecule combinant vectors, host cells (for producing the polymeptide), the secreted polymeptide (comprising a sequence of only A or T residues. Also included are secreted polymeptide fragment, domain, epitope, full-length protein, variant, allelic variant or species homologue), antibodies that secreted polymeptide fragment, domain, epitope, full-length protein, variant, allelic variant or species homologue), antibodies that specifically bind to the polymeptides, diagnosing, treating, preventing or ameliorating a medical condition by administering the polymenting or ameliorating an activity in a biological assay (by expressing the CDNA sequence and a biological assay and identifying the protein in the supernatant, and detecting an activity in a biological assay (by expressing the CC identifying an activity). The polymeptides, mucleic acids and antibodies are useful for diagnosing a pathological condition, such as cancer, inflammation and other immune activity, and polymeptides, mucleic acids and antibodies are useful for diagnosing apathological condition, such as cancer, inflammation and other immune disorders, neurological and blood clotting disorders (many examples are restriction mapping). The polymeptides are also useful for chromosome identification). The mucleic acids are also useful for chromosome identification, radiation hybrid mapping or long-range restriction apping the polymeptides are also ob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human secreted nucleic acid molecules and polypeptides, useful for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation, immune disorders, neurological and blood clotting
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Crocker PR;
                                                                                                                                                                                               2000US-0198407P.
2000US-0243792P.
2001US-00836353.
                                                                                                                          29-OCT-2001; 2001US-00984130
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LIU D.
CROCKER P R.
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KENNY J J.
OLSEN H S.
MOORE P A.
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M, Liu D,
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27-OCT-1999;
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Sequence 697 AA;

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                                                                                                                  61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
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                               Gaps
                             58;
   Length 697;
Score 3334; DB 6; Length 69
Pred. No. 3e-229;
0; Mismatches 1; Indels
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98.7%;
          Local Similarity 91.5
les 638; Conservative
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human; cell surface protein; immunoglobulin; BGS-19; cytostatic; gynaecological; immunosuppressive; antiinflammatory; antiasthmatic; antidiabetic; dermatological; gene therapy. Siglec-10 amino acid sequence SEQ ID NO:7. ADD26582 standard; protein; 697 15-JAN-2004 (first entry) Homo sapiens ADD26582;

WO2003083078-A2

61 FKAVTETTKGAPVATNHOSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120 FKAVTETTKGAPVATNHQSREVENSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120

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The present invention describes human cell surface protein with changolobulin folds, designated 856-19 (i). (I) has cytocatatic, communication describes human corp. antidiabetic and darmatological activities and can be used in gene cartification and dermatological activities and can be used in gene therapy. (I) can be used for preventing treating or ameliorating a medical condition, such as a disorder related to aberrant immunoglobulin receptor activity; adsorder; adisorder related to hyper- or hypo-lamunoglobulin receptor activity; adsorder; calacted to aberrant signal transduction; ar expendentive disorder; adisorder; related to hyper- or hypo-lamunoglobulin receptor activity; adisorder; an ovarian disorder; ovarian cancer; calacted to aberrant signal transduction; otherwise menopause; placemati dysfunction; infertility; pelyic inflammatory disease; candometricis; placental aroundates deficiency; premature menopause; placemati dysfunction; infertility; pelyic inflammatory disease; candometricis; incomplete isosexual precocity; premature showing of cender placematic premature puberty; percections; premature stowing of cendermatoric premature puberty; premature thelarch; premature puberty; premature thelarch; premature puberty; premature thelarch; premature puberty; premature thelarch; premature puberty; premature thelarch; premature puberty; premature thelarch; premature puberty; premature thelarch; premature puberty; premature thelarch; premature puberty; premature thelarch; premature puberty; premature thelarch; premature puberty; premature thelarch; premature puberty; premature thelarch; premature dysmenorrhoa; polymenorrhoa; polycytic oversus of inclammatory disorders; asthm; immune transplanted organs and tissues; such as high sorders; athmitis; granning and premature thelarch; protections to transplanted organs and tissues; such as high sorders; and premature infertility; adjoined and premature the special stored premature infertility; allomerulonpathics; such as T-cell medical cupical proposers; Musture
                                                                                                                                                                                                                                          New isolated nucleic acid molecule encoding BGS-19 polypeptides, useful for preventing, treating or ameliorating a medical condition, such as a disorder related to aberrant immunoglobulin cell surface receptor
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Pred. No. 3e-229;
0; Mismatches 1; Indels 5
                                                                                                                                                                Chen J;
                                                                                                                                                                Wu S,
                                                                                                                                                                                                                                                                                                                                                    Example 1; SEQ ID NO 7; 224pp; English.
                                                                                                                                                                Feder JN, Siemers NQ,
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                                       28-MAR-2003; 2003WO-US009676.
                                                                               28-MAR-2002; 2002US-0368422P.
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                                                                                                                                   181 TGAALSSQGTKPTTSHFSVLSFTPRPQDHNTDLTCHVDFSRKGVSVQRTVRLRVAYAPRD
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in the formation, differentiation and maintenance of multicellular corganisms. The fate of many individual cells (for example proliferation, or organisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information. The cells and the immediate environment. The information is often transmitted by secreted polypeptides (for example mitogenic factors, auryival factors, cytocoxic factors, differentiation factors, neuropeptides and hormones) which are received and interpreted by diverse cell receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interpreted by diverse and receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins of the invention may have cytostatic activities through the stimulation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or treating at tumour in a mammal. In addition, they may be useful for measuring or detecting the expression of a tumour associated gene. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242
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                                                                      to novel nucleic acids encoding human PRO secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 98.7%; Score 3334; DB 8; Length 6 Best Local Similarity 91.5%; Pred. No. 3e-229; Matches 538; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ERGSYVRYNFMNDGFFLKVT-------
                                     Claim 10; SEQ ID NO 10; 118pp; English.
                                                                         invention relates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention.
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The PRO proteins are useful for diagnosing and treating a B cell related disorder, e.g. X-linked infantile hypogammaglobulinemia, polyaacdaride antigen unresponsiveness, selective 19A deficiency, selective IgM proteince of the proteince of the proteince of the proteince of the proteince of the proteince of the protein in the protein protein in the protein protein in the protein in the protein in the protein in the protein in the protein in the protein in the protein in the protein in the protein in the protein in the protein in the protein in the protein in the development of the protein in the protein in the protein in the development of the protein in the development of the protein in the development of animals or knockout animals, which in turn are useful in the development and screening of therapeutically useful reagents.
New PRO polypeptide, useful for diagnosing and treating a B cell related disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
                                                                                                                                                                                                                              Immunosuppressive, Cytostatic, Antiarthritic, Antirheumatic, Antianemic, Antiale Ergic, Muscular, Neuroprotective, Nephrotropic, Antiinfiammatory, Gene Therapy, PRO, B cell related disorder, cancer; immune-mediated inflammatory disease, human.
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                                                             SOBELHYATLNFPGVRPRPBARMPKGTOADYABVKFO 697
                                        SQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ
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                                                                                                                            ADL82805 standard; protein; 697
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                                                                                                                                                                                                                                                                                                                                                                                               16-SEP-2002; 2002US-0411392P.
                                                                                                                                                                              (first entry)
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N-PSDB; ADL82804.
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                                                                                                                                                                                                      Human PRO71236,
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                                                                                                                                                    ADL82805;
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Wu TD;
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ADL82805
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241 LVISISRDNTPALEPQPQGNVPYLEAQKGQFIRLLCAADSQPPATLSWVLQNRVLSSSHP 300
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61 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
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                                                                                                                               ----VLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
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                                                                                     ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW
                                                                                                                                                                                                              LVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sialic acid-binding Ig-related lectin, Siglec-BMS-L3b.
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MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW 1 MILPLILSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW

98.7%; Score 3334; DB 8; Length 697; larity 91.5%; Pred. No. 3e-229; Conservative 0; Mismatches 1; Indels 58

Similarity

Local Best Loca Matches

Query Match

638;

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WPI; 2002-241565/29. N-PSDB; ABK43361 Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein molecules useful for treating immune system diseases such as asthma, leukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease.

Claim 5; Fig 3B; 209pp; English.

The Invention Feates to an isolated style. Feater compositions comprising (I) are useful for treating immune system diseases such as asthma, leukaemia or other allergic or inflammatory diseases. Extracellular domains of (I) represent potential markers for screening, diagnosis, prognosis, follow up assays, and imaging methods. (I) is useful as a target for drugs which inflammation, tissue damage and remodeling in asthma, and inflammatory diseases such as allergic rhinitis, osteoarthritis, Crohn's disease, psoriasis, rheumatoid arthritis, conjunctivitis, etc. (I) is also useful for monitoring the course of disease or disorders, and for identifying agents that bind with and/or modulate the biological activity of SIGLEC-BMS proteins. The nucleic acid molecules (II) encoding (I) are useful in diagnosis and/or prognosis methods, and to detect the presence and/or amount of SIGLEC-BMS uncleoside sequences and/or SIGLEC-BMS proteins and/or prognosis methods, and to detect the presence and/or amount of SIGLEC-BMS uncleoside sequences and/or signification of SIGLEC-BMS suchedial sample. (II) are useful as nucleic acid probes are useful for screening genomic library to isolate a genomic clone of SIGLEC gene. SIGLEC-BMS gene copy number is determined for detecting diseases or disorders associated with SIGLEC-BMS transcripts or proteins. The SIGLEC-BMS sutilodies are also used to detect, sont or isolate evels expressing SIGLEC-BMS proteeins and in diagnostic imaging technology. ABURG7074-AAU87089 represent human SIGLEC amino acid sequences of the The invention relates to an isolated SIGLEC (sialic acid-binding Ignvention ្នុងXង្គឹម្ពងក្នុងដើម្បីម៉ូស៊ីនិស្សកិច្ចិក្រពីពិភិបិតិ គឺគឺគឺគឺកិច្ចិក្ខិតិ ក្នុងក្នុងក្នុងក្នុងក្នុងក្នុង គឺ ក្នុង

Sequence 622 AA;

Gaps ., 97.7%; Score 3299; DB 5; Length 622; 100.0%; Pred. No. 8.1e-227; ive 0; Mismatches 0; Indels o 622; Conservative Query Match Best Local Similarity Matches 622; Conserv

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197 138 KVTVLSFIPRPQDHNIDLICHVDFSRKGVSAQRIVRLRVAYAPRDLVISISRDNTPALEP

240 258 GDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLENLGNGTSLPVLEGQS 198 QPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWWLQNRVLSSSHPWGPRPLGLELPGVKA 181 OPOGNVPYLEAQKGOFLRLLCAADSOPPATLSWVLONRVLSSSHPWGPRPLGLELPGVKA

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257

241 GDSGRYTCRAENRIGSQQRALDISVQYPPENLRVMVSQANRTVLENIGNGTSLPVLEGQS LCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQH 301 LCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQH 318

377

361 VSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPAPSLRWWLGEELLEGNSSQDSFEVT 378 VSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPAPSLRWWLGEELLEGNSSQDSFEVT

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420

438 PSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGSILQLPDXKGLISTAFSNGAFLG .21 PSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGSILQLPDKKGLISTAFSNGAFLG 498 IGITALLFLCLALIIMKILPKRRIQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKA 557

600 TPNSPRTPLPPGAPSPESKKNOKKOYOLPSFPEPKSSTQAPESQESQEELHYATLNFPGV 639 601 RPRPEARMPKGTQADYAEVKFQ RPRPEARMPKGTQADYAEVKFQ 558

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ADD19314 standard; protein; 710 AA.

15-JAN-2004 (first entry)

Human secreted protein from gene 18 #3.

human secreted protein, cytostatic, antibacterial, virucide, neuroprotective; gynaecological; gastrointestinal-Gen; cardiovascular-Gen; nephrotropic, antiinflammatory; muscular-Gen; respiratory-Gen; immunosuperssive; cerebroprotective; vasctropic, nootropic, antiallergic; cancer; bacterial infection; viral infection; muscular disorder; reproductive disorder; blood disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; inflammatory disorder; proliferative disorder; human

Homo sapiens

WO2003052377-A2.

26-JUN-2003

06-NOV-2002; 2002WO-US035606

07-NOV-2001; 2001US-0331046P.

(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Ruben SM;

WPI: 2003-533050/50. N-PSDB; ADD19239 New isolated nucleic acids encoding signal transduction pathway component polypeptides, useful for diagnosing, treating, and/or preventing disorders, such as cancer, infections, cardiovascular and inflammatory diseases

Claim 11; SEQ ID NO 141; 554pp; English

The invention relates to an isolated nucleic acid molecule (CDNA)

concoding a human secreted protein, representing one of 85 novel genes.

Also included are recombinant vectors, host cells (expressing the protein), the secreted proteins (including their fragments, epitopes and homologues), an isolated antibody that binds specifically to the protein, diagnosing a pathological condition or susceptibility to a pathological condition based on the presence of a mutation in the nucleic acid and diagnosing a condition based on the presence or absence of the mutation), diagnosing a pathological condition or susceptibility to a pathological condition (comprising determining the protein in a biological sample presence or amount of expression of the protein in a biological sample or and diagnosing a condition based on the presence or amount of expression of the protein in a biological condition of the protein in a biological sample of the protein to a mammalian subject, by administering the nucleic acid or protein to a mammalian subject, identifying a binding partner to the protein, the gene corresponding to the cDNA sequence, and identifying an activity in a biological assay (comprising expressing the nucleic acid in a cell, isolating the

(first entry)

05-JUN-2002

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QPQGNVPYLBAQKGQFLRILCAADSQPPATLSWVLQNRVLSSSHPWGPRPLGLELPGVKA 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQH 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQH 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSSAGFWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGSILQLPDKKGLISTAFSNGAFLG 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGSILQLPDKKGLISTAFSNGAFLG 568
supernatant, detecting an activity in a biological assay and identifying the protein in the supernatant having the activity). The nucleic acids and proteins display the following activities Cytostatic, antibacterial, Virucide, Neuroprotective, Gynaecological, Gastrointestinal-Gen, Cardiant, Gardiovascular-Gen, Nephrotropic, Antihilamatory, Muscular-Gen, Respiratory-Gen, Immunosuppressive, Carebroprotective, Vasotropic, Nootropic, Antialiargic. The methods and compositions of the present invention are useful for diagnosing, treating, preventing and/or prognosticating disorders related to the novel polypeptides, such as cancer, bacterial or viral infections, and neural, immune system, blood, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, remal, inflammatory or proliferative disorders (many examples of these diseases and disorders are given in the specification). The present sequence represents a novel secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                             VSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPAPSLRWWLGEELLEGNSSQDSFEVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 FLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSWTGAALSSQGTKPTTS
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                                                                                                                                                                                                                                                                                                                                                 61;
                                                                                                                                                                                                                                                                                                                 DB 7; Length 710;
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                                                                                                                                                                                                                                                                                                               Score 3174.5; DB 7;
Pred. No. 7.6e-218;
2; Mismatches 9;
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AAU87074 standard; protein; 544 AA

RESULT 13 AAU87074 ID AAU87

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The invention relates to an isolated SIGLEC (sialic acid-binding Igrelated lectin) protein (I). Pharmaceutical compositions comprising of are useful for treating immune system diseases such as asthma, leukaemia or other allergic or inflammatory diseases. Extracellular domains of (I) represent potential markers for screening, diagnosis, prognosis, following passays, and imaging methods. (I) is useful as a target for drugs which inhibit inflammation, tissue damage and remodeling in asthma, and inflammatory diseases such as allergic thinitis, osteoarthritis, crohn's disease, psoriasis, rheumatorid arthritis, conjunctivitis, etc. (I) is also useful for monitoring the course of disease or disorders, and for identifying agents that bind with and/or modulate the biological activity of SIGLEC-BMS proteins. The nucleic acid molecules (II) encoding (I) are useful in diagnosis and/or prognosis methods, and to detect the presence and/or amount of SIGLEC-BMS nucleotide sequences and/or SIGLEC-BMS proteins in a biological sample. (II) are useful as nucleic acid probes are useful for screening genomic library to isolate a genomic clone of signed cap and secreting diseases or disorders associated with SIGLEC-BMS transcripts or proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein molecules useful for treating immune system diseases such as asthma, leukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease
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                                                                                                                               Human, sialic acid-binding Ig-related lectin; SIGLEC; asthma; manne system disease, leukaemia; allergy; inflammatory disease; tissue damage; allergic rhinitis; osteoarthritis; Crohn's disease; psoriasis; rheumatoid arthritis; conjunctivitis.
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                                                                                              Sialic acid-binding Ig-related lectin, Siglec-BMS-L3a.
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llarity 85.1%; Pred. No. 1.7e-191;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Whitney G;
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N-PSDB; ABK43360.
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98US-0100038P
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21-APR-1998;
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                                                                                                                                                                                                                                                                                          241 HPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTV 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 GEELLEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCBAWNVHGAQSGSILQLP 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       541 NYVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPES 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, PRO, EST, expressed sequence tag, PCR primer, hybridisation, probe; blood coagulation disorder; cancer; cellular adhesion disorder; secreted protein; transmembrane protein.
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11-MAR-1998;
12-MAR-1998;
13-MAR-1998;
17-MAR-1998;
20-MAR-1998;
20-MAR-1998;
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506 QESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ 544

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The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood accordant and callular adhesion disorders. They may also be used to raise antibodies, AAZ31891 to AAZ34388, and AAY41685 to AAY41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERGSYVTYNFMNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLKVAYAP
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                                                                                                                                          New secreted and transmembrane polypeptides and their polynucleotides, useful for treating blood coagulation disorders, cancers and cellular adhesion disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        387 -KKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYI
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84.8%; Pred. No. 1.4e-190;
ive 0; Mismatches 2; Indels 95;
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                                                    Baker
                                                    Yuan J,
                                                                                                                                                                                                                  Claim 12; Fig 93; 530pp; English.
                                                     Gurney A,
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Matches 542; Conservative
               GETH ) GENENTECH INC.
                                                    Goddard A,
                                                                                      WPI; 1999-551358/46
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AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bicactive molecules to cells and for modulating biclogical activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide provide specific targeting of bicactive molecules to cells. AAC78600 to AAC78897 represent PCR primers and probes used in the isolation of the PRO polynucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel PRO polypeptides and polynucleotides used in detection methods, target bioactive molecules to specific cells, and to modulate cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I, Gerritsen ME;
'Hillan KJ;
Roy MA, Shelton
                                                                                                                 Human, secreted protein; transmembrane protein, PRO, BST; cytostatic, expressed sequence tag, detection, cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eaton DL;
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E, Fong S, Gao W, Gerber H,
Ju, Crimaldi CJ, Gurney AL, 'H
Napier MA, Pan J, Paoni NF,
Williams PM, Wood WI;
                                                                                            Human PRO940 (UNQ477) protein sequence SEQ ID NO:259
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              AAB44280 standard; protein; 544
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990S-0134287P.
990S-0141037P.
99US-0145698P.
99US-0162506P.
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99US-0123957P.
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Filvaroff E, 1
Godowski PJ, C
Kuo SS, Napi
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14-MAY-1999;
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26-JUL-1999;
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Goddard A,
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Query Match 82.6%; Score 2790.5; DB 3; Length 544;
Best Local Similarity 84.8%; Pred. No. 1.4e-190;
Matches 542; Conservative 0; Mismatches 2; Indels 95; Gaps
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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Title: Perfect score:

US-09-937-636-4 3377 1 MILPLILSSLIGGSQAMDGR......RPEARMPKGTQADYAEVKFQ 639

Sequence:

Scoring table:

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2002273 seqs, 358729299 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	31023 Aaw81023 Human sie	543 Aay97543	580 Aab25580	27052 Auman nov	5582 Ade86582	97087 . Aau87087 Sialic ac	7153 Ada27153	Add26582	Adi37010	ADL82805 Human PRO	Aau87075	14 Add19314	AAU87074 Aau87074 Sialic ac	724	•	AAU29082 Aau29082 Human PRO	3458 Abu58458 Human	Abu88006	N	g	3585 Abr65585	525 Abu99525	82764 Human PRO	
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ABU96187	ABU92618	AB008695	AB002747	ABR74901	ABR94663	AB025226	ABU85636	ABU98796	ABU98011	ABU91717	ABU72232	ABU89410	ABU86251	ABU67464	ABU80492	ABR99410	ABR98800	AB016323	ABR92223
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ALIGNMENTS

AAW81023 standard; protein; 639 AA RESULT 1 AAW81023

AAW81023;

(first entry) 26-APR-1999 Human sialoadhesin family 4 (SAF-1) polypeptide

SAF-4; staloadhesin family; human; therapy; diagnosis; cancer; inflammation; autoimmune disease; allergy; asthma; inflammation; cerebellar degeneration; Alzheimer's disease; Parkinson's disease; multiple sclerosis, amyotrophic lateral sclerosis; head injury; septic shock; sepsis; stroke; osteoporosis; osteoarthritis; lischemia repertusion injury; cardiovascular disease; kidney disease; liver disease; myocardial infarction; hypotension; hypertension; AIDS; myelodysplastic syndrome; aplastic anaemia; baldness; infection.

Homo sapiens.

WO9853840-A1

03-DEC-1998.

98WO-US010791. 27-MAY-1998; 97US-0047572P. 27-MAY-1997; (SMIK) SMITHKLINE BEECHAM CORP.

Kikly KK, Erickson-Miller CL;

WPI; 1999-080779/07. N-PSDB; AAV99911.

t C New sialoadhesin family 4 polypetides and polynucleotides - useful treat various diseases associated with SAF-4 expression.

Claim 1; Page 31; 48pp; English.

This is the amino acid sequence of new human sialoadhesin family 4 (SAF-4), as deduced from the nucleotide sequence of an isolated cDNA clone (see AAV99911). SAF-4 polynucleotides and polypetides, and methods for producing such polypetides in transformed host cells using recombinant techniques are disclosed. SAF-4, its agonists and antagonists, and nucleic acid molecules that enhance or inhibit SAF-4 expression, may be used to treat patients in need of enhancement or inhibition of SAF-4

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expression or activity. Conditions that may benefit from such treatment archaet cancer, inflammation, autocimmunity, allergy, asthma, rheumatoid archaettis, CNS inflammation, cerebellar degeneration, Althelmer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, head injury damage and other neurological disorders, septic shock, sepsis, stroke, osteoporosis, osteoarthrifs, isofemmia reperfusion injury, cardiovascular disease, kidney disease, liver disease, isohemic injury, myocardial infarction, hypotension, hypertension, AlDS, myelodysplastic syndromes and other heematologic abnormalities, aplastic anaemia, male baldness pattern and bacterial, protozoal, fungal and viral infections related to SAF-4 polypeptide activity. Methods of identifying agonistic assays for detecting diseases associated with inappropriate SAF-4 activity or levels
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Ą AAY97543 ID AAY97543 standard; protein; 639 AAY97543; RESULT 2

(first entry)

12-FEB-2001

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This sequence is a human obesity protein binding protein-2 homologue (hobbensh) of the invention. The hOB-BP2h nucleic acids and polypeptides may be used for the manufacture of a medicament for the treatment of obesity and/or obesity-related disorders. The hOB-BP2h nucleic acids are useful as probes or amplification primers in the detection, quantification or isolation of gene sequences or transcripts, for recombinant expression of hOB-BP2h polypeptides, as immunogens in the preparation and screening of antibodies, and in sense or antisense suppression of one or more hOB-BP2h antibodies and in sense or antisense suppression of one or more hOB-BP2h Antigenic epitope-bearing peptides and polypeptides are useful for raising or screening antibodies that specifically binds to the hOB-BP2h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERGSYVRYNFMNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP
                                             Human obesity protein binding protein-2 homologue; hOB-BP2h; obesity, obesity,related disorder; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERGSYVRYNFMNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP
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medicament for
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                                                                                                                                                                                                                                                                                                                                                                                            New human obesity protein binding protein-2 homologue polynucleotides and polypeptides useful for producing treating obesity and/or obesity-related disorders.
            Human obesity protein binding protein-2 homologue #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 3377; DB 3;
100.0%; Pred. No. 2.3e-232;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; Page 89-91; 92pp; English
                                                                                                                                                                                                    22-MAR-2000; 2000WO-US006682.
                                                                                                                                                                                                                                       99US-0127667P
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639, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 639 AA;
                                                                                                                                   WC200059942-A2
                                                                                                                                                                                                                                                                                                            Wei J;
                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                        02-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptides
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Best Local S:
Matches 639,
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241 HPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTV 300

LENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVE 361 HEGEFTCHARHPLGSQHVSLSLSVHYSPKLLGPSCSWEAEGLHCSCSSQASPAPSLRWWL

301 301

HPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTV

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AAV99912 standard; cDNA; 3099 BP. AAV99912;

(first entry) 26-APR-1999

Human sialoadhesin family 4 (SAF-1) related EST clone.

SAF-4; sialoadhesin family; human; therapy; disgnosis; cancer; inflammation; autoimmune disease; allergy; asthma; inflammation; cerebellar degeneration; Alzheimer's disease; Parkinson's disease; multiple sclerosis, amyotrophic lateral sclerosis; head injury; septic shock; sepsis; stroke; oateoporosis; osteoathritis; ischman reperfusion injury; cardiovascular disease; kidney disease; liver disease; myccardial infarction; hypotension; hypotension; AlDS; myelodysplastic syndrome; aplastic anaemia; baldness; infection; ss.

Homo sapiens.

/*tag= a /transl_except= (pos:1176. .1177, aa:Pro) /note= "this codon has an apparent 1 nucleotide deletion which alters the reading frame" Location/Qualifiers . .1249

WO9853840-A1

98WO-US010791. 27-MAY-1998; 97US-0047572P. 27-MAY-1997; (SMIK) SMITHKLINE BEECHAM CORP

Erickson-Miller CL; Kikly KK,

1999-080779/07.

New sialoadhesin family 4 polypetides and polynucleotides - useful treat various diseases associated with SAF-4 expression.

Claim 13; Page 31-32; 48pp; English.

This is the nuclectide sequence of an expressed sequence tag (EST) clone that encodes a polypeptide (see AAM81024) which shows close homology and/or structural similarity (e.g. a conservative amino acid difference) to new human slanladather family 4 (SAF-4) polypeptide (see AAW81023). SAF-4 polynuclectides and polypeptides, and methods for producing such polypeptides in transformed host cells using recombinant techniques, are disclosed. SAF-4, its agonists and artagonists, and nucled acid antended that enhance or inhibit SAF-4 expression, may be used to treat patients in need of enhancement or inhibit ton of SAF-4 expression or activity. Conditions that may benefit from such treatment include cancer, inflammation, cerebellar degeneration, Alzehimer's disease, Parkinson's clinifarmation, autoimmunity, allergy, asthma, richamatoid arthritis, CNS inflammation, cerebellar degeneration, Alzehimer's disease, Parkinson's disease, wultiple sclerosis, amyotrophic lateral sclerosis, head injury damage and other neurological disorders, septic shock, sepsis, stroke, osteoporosis, osteobarthritis, ischemia reperfusion injury, myocardial inflatoriton, hypoentanison, AIDS, myelodypalatic syndam, ame balaness pattern and bacterial, protozoal, fungal and viral inflections related to safe-4 polypeptide activity. Methods of identifying agonists, safety or antagonists/inhibitors are also provided, as well as diagnostic assays for electing diseases associated with inappropriate SAF-4 activity or antagonists or antagonists or antagonists or antagonists or antagonist

Sequence 3099 BP; 770 A; 907 C; 813 G; 607 T; 0 U; 2 Other;

ó 951 CTGGAAAACCTTGGGAACGGCACGTCTCTCCCAGTACTGGAGGGCCAAAGCCTGTGCCTG 1010 961 GTCTGTGTCACACACAGCAGCCCCCCAGGCTGAGCTGGACCCAGAGGGGACAAGGTT 1020 1021 CTGAGCCCCTCCCAGCCCTCAGACCCCGGGGTCCTGGAGCTGCCTCGGGTTCAAGTGGAG 1080 180 240 300 540 009 650 999 720 780 830 840 890 900 950 960 110 120 170 230 290 350 360 410 420 470 480 530 590 710 770 09 TGCTCTTTCTCCTACCCCCGACAAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGG GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGGCCAAGGGGAAC 411 GAGAGGAAGCTATGTGAGATATATTTCATGAACGATGGGTTCTTTTTAAAAGTAACA TCTGTGCAGTATCCTCCAGAGACCTGAGAGTGATGGTTTCCCCAAGCAAACAGGACAGTC 111 Trendanacaagracaagaagraangangangengeegagagagaganererengee TGCTCTTTCTCCTACCCCCGACAAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGG 231 TTCAAAGGAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACCACAGAGTGGT TGCTCCTTGGTGATCAGAGGCGCAGATGCAGGATGAGTCACAGTACTTCTTTCGGGTG TTCTCCAGAAAGGGTGTGAGCGCACACAGAGGACGGTCCGACTCCGTGTGGGCCTATGCCCCC 591 AGAGACCTIGITATCAGCATTTCACGTGACAACACGCCAGCCCTGGAGCCCCAGCCCCAG 601 GGAAATGTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGCGGCTCCTCTGTGCTGCT GACAGCCACCCCTGCCACACTGAGCTGGGTCCTGCAGAACAGAGTCCTCCTCGTCC 771 CATCCTGGGGCCCTAGACCCCTGGGCTGGAGCTGCCCGGGGTGAAGGCTGGGGATTCA GGGCGCTACACCTGCCGAGCGGAGACAGGCTTGGCTCCCAGCAGCGAGCCTGGACCTC 831 GGGCGCTACACCTGCCGAGCGGAGCAGCTTGGCTTCCCAGCAGCGAGCCTGGACCTC rengingeagranecreagagaacergagagigargarigginineecaageaaacagaacagic GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAC CTAAAAGTAACA GTGCTCAGCTTCACGCCCAGACCCCAGGACCACAACACCGACCTCACCTGCCATGTGGAC grecticaectricaceccasaccccassaccacaccacaccaccaccaccacctaccaccateres GGAAATGTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGCGGGGTCCTCTGTGCTGCT CATCCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGGTGAAGGCTGGGGATTCA TTCTGGATACGAGTGCAGGAGTCAGTGATGGTGCCGGAGGGCCTGTGTGCATCTCTGTGCCC TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACCACAGAGTCGA Gaps ; 0 Length 3099; Indels 1 AIGCIACIGCCACIGCIGCIGICCICCICGCIGCIGGCGGGGGCCCCAGGC GAGAGGAAGCTATGTGAGATATAATTTCATGAACGATGGGTTCTT DB 2; ; 0 100.0%; Score 1917; 100.0%; Pred. No. 0; ive 0; Mismatches Query Match Best Local Similarity 100.0 Matches 1917; Conservative 541 7 891 661 121 181 481 841 901 301 651 721 781 241 291 361 421 471

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                                                                           1141 AGCCTCTCGGGGCACTACTCCCCGAAGCTGGTGGGGCCCCTCCTGCTCCTGGGAGGCTGAG 1200
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AAV99911 standard; cDNA; 3099 BP. 26-APR-1999 AAV99911; RESULT 3 AAV9991 axaxaxaxa A

Human sialoadhesin family 4 (SAF-1) cDNA. (first entry)

SAF-4; sialoadhesin family; human; therapy; diagnosis; cancer; inflammation; autoimmune disease; allergy; asthma; inflammation; ecrebellar degeneration; Alzheimer's disease; Parkinson's disease;

171 TGCTCTTTCTCCTACCCCCGACAAGACTGGACAGGGTCTACCCCCAGCTTATGGCTACTGG 230

셤 ð

121 TECTOTITOTOCOCOCOCOCACAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGG 180

This cDNA clone codes for new human stalcadhesin family 4 (SAF-4)
polypeptide (See AAM81023). It can be obtained e.g. from a CDNA library
carived from mRNA in cells of human primary dendritic cells, using
expressed sequence tag analysis. SAP-4 polymocleotides and polypeptides
and methods for producing such polypeptides by recombinant techniques are
and methods for producing such polypeptides by and mucleic acid
acidsclosed. SAF-4, its agonists and antegonists, and mucleic acid
molecules that enhance or inhibit SAF-4 expression, may be used to treat
patients in need of enhancement or inhibition of SAF-4 expression or
carivity. Conditions that may benefit from such treatment include cancer,
inflammation, autoimmunity, allergy, atthma, rheumatoid arthritis. CNS
inflammation, cereballar degeneration, Alzheimer's disease, head injury
damage and other neurological disorders, septic shock, sepsis, stroke,
disease, miltiple solerosis, amyorders, septics shock, sepsis, stroke,
disease, kidney disease, liver disease, ischemia reperfusion injury, cardiovascular
disease, kidney disease, liver disease, ischemic injury, myocardial
infarction, hypotension, hypertension, AlDS, myelodysplastic syndiess
con other haematologic abnormalities, achemic mademia, male baldness
contended the pathods of identifying agonists,
she hypotension, and servivery Methods of identifying agonists,
she hypotension, and servivery methods, as well as diagnostic assays
for detecting diseases associated with inappropriate SAF-4 activity or ö TTCTGGATACGAGTGCAGGAGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCC 120 septic shock, sepsis, stroke, osteoporosis, osteoarthritis, ischemia reperfusion injury; cardiovascular disease, kidney disease, liver disease, myocardial infarction; hypotension; hypertension; AIDS, myelodysplastic syndrome; aplastic anaemia; baldness; infection; ss. New sialcachesin family 4 polypetides and polynucleotides - useful to treat various diseases associated with SAF-4 expression. Gaps . 0 multiple sclerosis, amyotrophic lateral sclerosis; head injury; 100.0%; Score 1917; DB 2; Length 3099; 100.0%; Pred. No. 0; iive 0; Mismatches 0; Indels 0; Sequence 3099 BP; 769 A; 908 C; 813 G; 607 T; 0 U; 2 Other; Location/Qualifiers 51. .1970 Claim 2; Page 30-31; 48pp; English. (SMIK) SMITHKLINE BEECHAM CORP. Kikly KK, Brickson-Miller CL; 97US-0047572P. 98WO-US010791 Best Local Similarity 100.0 Matches 1917; Conservative /*tag≈ a 1999-080779/07. P-PSDB; AAW81023 Homo sapiens. WO9853840-A1. 27-MAY-1998; 27-MAY-1997; 61 Query Match levels g δ ద This Page Blank (uspto)